

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2004, 04:28:27 ; Search time 78 Seconds

(without alignments)
2835.038 Million cell updates/sec

Title: US-09-315-355C-10

Perfect score: 501
Sequence: 1 MNRSRQVTCVAMVRCGVAKL.....RNSISGPGFSRSSDTPMES 501

Scoring table:

OLIGO	Xgapop 60.0	Xgapext 60.0
	Ygapop 60.0	Ygapext 60.0
	Fgapop 6.0	Fgapext 7.0
	Delop 6.0	Delext 7.0

Searched: 569978 seqs, 220691566 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1135299

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-O=/cgnt2_1/USPRO.spool_D/US09315355/runat_30012004_091942_24664/app_query.fasta_1.647
-DB=Issued_Patents_NA -OPMT=fastcap -SUFFIX=olip2n.rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=numan40.cdi
-LIST=45 -DOCMALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09315355 @CGN 1.1 85 @runat_30012004_091942_24664 -NCPU=6 -ICPU=3
-NO MMAR -LARGEOUTRY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARR_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=30 -DELOP=6 -DELEXT=7

Database: Issued Patents NA:*

1:	/cgnt2_6/ptodata/2/ina/5A.COMB.seq:*
2:	/cgnt2_6/ptodata/2/ina/5B.COMB.seq:*
3:	/cgnt2_6/ptodata/2/ina/6A.COMB.seq:*
4:	/cgnt2_6/ptodata/2/ina/6B.COMB.seq:*
5:	/cgnt2_6/ptodata/2/ina/PTUS.COMB.seq:*
6:	/cgnt2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	10	2.0	555	4 US-09-449-285A-15	Sequence 15, Appli
C 2	10	2.0	10380	3 US-09-077-354B-3	Sequence 3, Appli
C 3	9	1.8	321	2 US-08-520-678A-23	Sequence 23, Appli
C 4	9	1.8	321	3 US-08-897-126-23	Sequence 23, Appli
C 5	9	1.8	356	2 US-08-520-678A-22	Sequence 22, Appli
C 6	9	1.8	356	3 US-08-897-126-22	Sequence 22, Appli
C 7	9	1.8	1248	4 US-09-489-847-101	Sequence 101, App
C 8	9	1.8	1603	3 US-09-009-443-11	Sequence 11, Appli
C 9	9	1.8	1702	3 US-09-413-574-3	Sequence 3, Appli
C 10	9	1.8	1705	4 US-09-205-258-216	Sequence 216, App
C 11	9	1.8	1977	4 US-08-705-477E-99	Sequence 99, Appli
C 12	9	1.8	2073	3 US-09-032-523-6	Sequence 6, Appli

13	9	1.8	2232	4 US-09-581-831-1	Sequence 1, Appli
C 14	9	1.8	2867	4 US-09-402-532-38	Sequence 38, Appli
C 15	9	1.8	5864	3 US-08-482-918-47	Sequence 47, Appli
C 16	9	1.8	5864	3 US-09-224-681-47	Sequence 47, Appli
C 17	9	1.8	5864	3 US-08-336-728A-47	Sequence 47, Appli
C 18	9	1.8	9278	1 US-08-243-542-9	Sequence 9, Appli
C 19	9	1.8	9278	1 US-08-477-407-9	Sequence 9, Appli
C 20	9	1.8	9278	1 US-08-484-355-9	Sequence 9, Appli
C 21	9	1.8	9646	3 US-08-811-566-1	Sequence 1, Appli
C 22	9	1.8	9646	3 US-09-034-756-1	Sequence 1, Appli
C 23	9	1.8	9704	4 US-09-814-951A-3	Sequence 3, Appli
C 24	9	1.8	11811	3 US-09-078-294-7	Sequence 7, Appli
C 25	9	1.8	12980	3 US-08-811-566-5	Sequence 5, Appli
C 26	9	1.8	12980	4 US-09-034-756-5	Sequence 5, Appli
C 27	9	1.8	23187	4 US-09-499-522-1	Sequence 1, Appli
C 28	9	1.8	35060	3 US-08-814-095-7	Sequence 7, Appli
C 29	9	1.8	42571	4 US-09-810-347-3	Sequence 3, Appli
C 30	9	1.8	55827	4 US-09-813-133A-3	Sequence 3, Appli
C 31	9	1.8	80246	3 US-09-078-294-4	Sequence 4, Appli
C 32	9	1.8	80595	3 US-09-078-294-3	Sequence 3, Appli
C 33	9	1.8	246240	2 US-08-724-394A-20	Sequence 20, Appli
C 34	9	1.8	246240	2 US-08-724-394A-21	Sequence 21, Appli
C 35	9	1.8	246240	2 US-08-724-394A-22	Sequence 22, Appli
C 36	9	1.6	40	3 US-09-306-290-26	Sequence 26, Appli
C 37	8	1.6	54	2 US-08-771-624B-24	Sequence 24, Appli
C 38	8	1.6	144	2 US-08-747-121-2	Sequence 2, Appli
C 39	8	1.6	187	4 US-09-702-705-1474	Sequence 1474, Ap
C 40	8	1.6	187	4 US-09-736-457-1474	Sequence 1474, Ap
C 41	8	1.6	247	4 US-09-397-787-79	Sequence 79, Appli
C 42	8	1.6	337	5 PCT-US91-06234A-2	Sequence 2, Appli
C 43	8	1.6	342	4 US-09-056-556-219	Sequence 219, App
C 44	8	1.6	342	4 US-09-072-596-214	Sequence 214, App
C 45	8	1.6	440	4 US-08-579-445-27	Sequence 27, Appli

ALIGNMENTS

RESULT 1

US-09-449-285A-15/c
; Sequence 15, Application US/09449285A

Patent No. 6113280

GENERAL INFORMATION:

; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnologie

; TITLE OF INVENTION: SMAD-INTERACTING POLYPEPTIDES AND THEIR USE

; FILE REFERENCE: 2676-4232US

; CURRENT APPLICATION NUMBER: US/09/449, 285A

; CURRENT FILING DATE: 1999-11-24

; PRIOR APPLICATION NUMBER: PCT/EP98/03193

; PRIOR FILING DATE: 1998-05-28

; PRIOR APPLICATION NUMBER: 97201645.5

; PRIOR FILING DATE: 1997-06-02

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 15

; LENGTH: 555

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (382)..(555)

; OTHER INFORMATION: n can be any nucleotide

US-09-449-285A-15

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-09-315-355C-10 (1-501) x US-09-449-285A-15 (1-555)

Length: 555

Matches: 10

Conservative: 0

Mismatch: 0

Indels: 0

Gaps: 0

QY 236 SerLysLysSerLysLysLysLysLys 245
|||||
Db 31 TCAGAACTGTCAGAAAAAAAAAAAAAAAAAAAA 2

RESULT 2
US-09-077-354B-3
; Sequence 3, Application US/09077354B
; Patent No. 6255096
; GENERAL INFORMATION:
; APPLICANT: HOPWOOD, JOHN JOSEPH; SCOTT, HAMISH STEELE;
; APPLICANT: WEBER, BIRGIT, BLANCH, LIANNE; ANSON, DONALD STEWART
; TITLE OF INVENTION: SYNTHETIC MAMMALIAN
; TITLE OF INVENTION: '-N-ACETYLGLUCOSAMINIDASE AND GENETIC SEQUENCES ENCODING SAME
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: UNITED STATES
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077.354B
; FILING DATE: 22-APRIL-1999
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00747
; FILING DATE: 22-NOV-1996
; ATORNEY/AGENT INFORMATION:
; NAME: POKALSKI, ANN R.
; REGISTRATION NUMBER: 34,697
; REFERENCE/DOCKET NUMBER: 12416
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516 742 4343
; TELEFAX: 516 742 4366
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10380 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Chromosome 17
; FEATURE:
; NAME/KEY: exon 1
; LOCATION: 990..1372
; FEATURE:
; NAME/KEY: exon 2
; LOCATION: 2115..2262
; FEATURE:
; NAME/KEY: exon 3
; LOCATION: 3056..3202
; FEATURE:
; NAME/KEY: exon 4
; LOCATION: 3387..3472
; FEATURE:
; NAME/KEY: exon 5
; LOCATION: 5667..5923
; FEATURE:
; NAME/KEY: exon 6
; LOCATION: 7745..8955
; US-09-077-354B-3

Alignment Scores:
Pred. No.: 17.6 Length: 10380
Score: 10.00 Matches: 10

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.00%
DB: 3 Gaps: 0

US-09-315-355c-10 (1-501) x US-09-077-354B-3 (1-10380)

QY 239 SerLysLysLysLysLysLysLysLys 248
|||||
Db 4829 TCAGAACTGTCAGAAAAAAAAAGGAGAGAAA 4858

RESULT 3
US-08-520-678A-23/c
; Sequence 23, Application US/08520678A
; Patent No. 5874565
; GENERAL INFORMATION:
; APPLICANT: Rice, Charles M.
; APPLICANT: Kolykhalov, Alexander A.
; TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
; TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howell & Haferkamp, L.C.
; STREET: 7733 Forsyth Blvd., Suite 1400
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520.678A
; FILING DATE:
; CLASSIFICATION: 536
; ATORNEY/AGENT INFORMATION:
; NAME: Henderson, Melodie W.
; REGISTRATION NUMBER: 37,848
; REFERENCE/DOCKET NUMBER: 6029-6836
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; TELEX:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 321 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-520-678A-23

Alignment Scores:
Pred. No.: 5.68 Length: 321
Score: 9.00 Matches: 9
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 1.80%
DB: 2 Gaps: 0

US-09-315-355c-10 (1-501) x US-08-520-678A-23 (1-321)

QY 240 LysLysLysLysLysLysLysLysLys 248
|||||
Db 162 AAAAAAAAAAAAAAAAAAGGAGAGAAA 136

RESULT 4
US-08-897-126-23/c
; Sequence 23, Application US/08897126
; Patent No. 6297003
; GENERAL INFORMATION:

APPLICANT: Rice, Charles M.
APPLICANT: Kolykhalov, Alexander A.
TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Hafeerkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
CITY: St. Louis
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,126
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/520,678
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Henderson, Melodie W.
REGISTRATION NUMBER: 37,848
REFERENCE/DOCKET NUMBER: 6029-6836
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
TELEX:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-897-126-23

Alignment Scores:
Pred. No.: 5.68 Length: 321
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservatave: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
Gaps: 0

US-09-315-355C-10 (1-501) x US-08-897-126-23 (1-321)

QY 240 LysLysLysLysLysLysGlyLysLys 248
Db 162 AAAAAAAAAAAAAAAAAAGGAAAAAAA 136

RESULT 5
US-08-520-678A-22/C
Sequence 22, Application US/08520678A
GENERAL INFORMATION:
APPLICANT: Rice, Charles M.
APPLICANT: Kolykhalov, Alexander A.
TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Hafeerkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
CITY: St. Louis
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,678A
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Henderson, Melodie W.
REGISTRATION NUMBER: 37,848
REFERENCE/DOCKET NUMBER: 6029-6836
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
TELEX:
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-520-678A-22

Alignment Scores:
Pred. No.: 6.28 Length: 356
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservatave: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
Gaps: 0

US-09-315-355C-10 (1-501) x US-08-520-678A-22 (1-356)

QY 240 LysLysLysLysLysLysGlyLysLys 248
Db 216 AAAAAAAAAAAAAAAAAAGGAAAAAAA 190

RESULT 6
US-08-897-126-22/C
Sequence 22, Application US/08897126
GENERAL INFORMATION:
APPLICANT: Rice, Charles M.
APPLICANT: Kolykhalov, Alexander A.
TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF HEPATITIS
TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Hafeerkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
CITY: St. Louis
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,126
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/520,678
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Henderson, Melodie W.
REGISTRATION NUMBER: 37,848
REFERENCE/DOCKET NUMBER: 6029-6836
TELECOMMUNICATION INFORMATION:

TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 356 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-897-126-22

Alignment Scores:
Pred. No.: 6.28 Length: 356
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
DB: 3 Gaps: 0

US-09-315-355C-10 (1-501) x US-08-897-126-22 (1-356)

Oy 240 LysLysLysLysLysLysLysLysLysLysLysLys 248
Db 216 AAAAAAAAAAAAAAAAAAGAAAAA 190

RESULT 7
US-09-489-847-101
Sequence 101, Application US/09489847
Patent No. 6476195
GENERAL INFORMATION:
APPLICANT: Rosen et al
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: P2031p1
CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/096,319
EARLIER FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER FILING DATE: 1998-08-06
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 376
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 101
LENGTH: 1248
TYPE: DNA
ORGANISM: Homo sapiens
US-09-489-847-101

Alignment Scores:
Pred. No.: 21.2 Length: 1248
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
DB: 4 Gaps: 0

US-09-315-355C-10 (1-501) x US-09-489-847-101 (1-1248)

Oy 237 LysLysLysLysLysLysLysLysLysLysLysLys 245
Db 1154 AACTCTCAAAAAAAAAAAAAAAAAA 1180

RESULT 8
US-09-009-443-11
Sequence 11, Application US/09009443

Patent No. 6259003
GENERAL INFORMATION:
APPLICANT: Fujisawa, Koichi
APPLICANT: Kaekabe, Yoshinisa
APPLICANT: Nishiguchi, Susumu
APPLICANT: Maekawa, Yoshiniko
APPLICANT: Allen, Randy Dale
TITLE OF INVENTION: PLANT PROMOTERS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 2000 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,443
FILING DATE: 20-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Mays, Thomas D.
REGISTRATION NUMBER: 34,524
REFERENCE/DOCKET NUMBER: 20455-20113.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/887-1500
TELEFAX: 202/887-0763
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1603 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: *Gossypium barbadense*
TISSUE TYPE: seedling
IMMEDIATE SOURCE:
CLONE: GKC22
US-09-009-443-11

Alignment Scores:
Pred. No.: 27 Length: 1603
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
DB: 3 Gaps: 0

US-09-315-355C-10 (1-501) x US-09-009-443-11 (1-1603)

Oy 241 LysLysLysLysLysLysLysLysLysLysLysLys 249
Db 403 AAAAAAAAAAAAAAAAAAGAGACT 429

RESULT 9
US-09-413-574-3
Sequence 3, Application US/09413574
Patent No. 6235972
GENERAL INFORMATION:
APPLICANT: Mahajan, Pramod B.
APPLICANT: Taghiani, Laura
TITLE OF INVENTION: Maize Rad23 Genes and Uses Thereof
FILE REFERENCE: 0964
CURRENT APPLICATION NUMBER: US/09/413,574
CURRENT FILING DATE: 1999-10-06
EARLIER APPLICATION NUMBER: 60/109,728
EARLIER FILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 5

```
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1702
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (106)...(1209)
US-09-413-574-3

Alignment Scores:
Pred. No.: 28.7 Length: 1702
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
DB: 3 Gaps: 0

US-09-315-355C-10 (1-501) x US-09-413-574-3 (1-1702)
Oy 237 LysleuSerLysLysLysLysLys 245
Db 1670 AACTTATCTAATAAAAAAAAAAAAAA 1696

RESULT 10
US-09-205-258-216
; Sequence 216, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007p1
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: US/09/205,258
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
```

```
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 216
; LENGTH: 1705
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1281)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1704)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-216

Alignment Scores:
Pred. No.: 28.7 Length: 1705
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
DB: 4 Gaps: 0

US-09-315-355C-10 (1-501) x US-09-205-258-216 (1-1705)
Oy 237 LysleuSerLysLysLysLysLys 245
Db 1643 AACTGTCAAAAAAAAAAAAAAAAAA 1669

RESULT 11
US-08-705-477E-99
```

Sequence 99, Application US/08705477E
Patent No. 6569432
GENERAL INFORMATION:
APPLICANT: Israel, Ron S.
APPLICANT: Heaton, Warren D.W.
APPLICANT: Fair, William R.
APPLICANT: Overfelli, Quathak
APPLICANT: Pinto, John
TITLE OF INVENTION: PROSTATE-SPECIFIC MEMBRANE ANTIGEN AND USES THEREOF
FILE REFERENCE: 1769/41426-G
CURRENT APPLICATION NUMBER: US/08/705,477E
CURRENT FILING DATE: 1996-08-29
NUMBER OF SEQ ID NOS: 128
SOFTWARE: PatentIn version 3.1
SEQ ID NO 99
LENGTH: 1977
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (840)..(843)
OTHER INFORMATION: n=any nucleotide
FEATURE:
NAME/KEY: misc feature
LOCATION: (1294)..(1295)
OTHER INFORMATION: n=any nucleotide
FEATURE:
NAME/KEY: misc feature
LOCATION: (1338)..(1343)
OTHER INFORMATION: n=any nucleotide
FEATURE:
NAME/KEY: misc feature
LOCATION: (1965)..(1966)
OTHER INFORMATION: n=any nucleotide
FEATURE:
NAME/KEY: misc feature
LOCATION: (1096)..(1101)
OTHER INFORMATION: n=any nucleotide
US-08-705-477E-99

Alignment Scores:
Pred. No.: 33.1 Length: 1977
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
DB: 4 Gaps: 0

US-09-315-355C-10 (1-501) x US-08-705-477E-99 (1-1977)

OY 240 LysLysLysLysLysLysGlyLysLys 248
Db 1786 AAAAAAAAAAAAAAAAAAGCGAAAAA 1812

RESULT 1:
US-09-033-523-6
Sequence 6, Application US/09032523
Patent No. 6232454
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl
APPLICANT: Baugh, Mariah
TITLE OF INVENTION: HUMAN PROTEINASE MOLECULES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,523
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0479 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2073 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PANTCTUT01
CLONE: 1515165
US-09-032-523-6

Alignment Scores:
Pred. No.: 34.7 Length: 2073
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
DB: 3 Gaps: 0

US-09-315-355C-10 (1-501) x US-09-032-523-6 (1-2073)

OY 240 LysLysLysLysLysLysGlyLysLys 248
Db 2007 AAAAAAAAAAAAAAAAAAGGAAAAAAG 2033

RESULT 13
US-09-581-831-1
Sequence 1, Application US/09581831
Patent No. 6448020
GENERAL INFORMATION:
APPLICANT: TOFTGARD, RUNE
APPLICANT: ZAPHIROPOULOS, PETER G.
APPLICANT: KOSERMAN, PRIIT
APPLICANT: GRIMM, THOMAS
TITLE OF INVENTION: MOLECULES ASSOCIATED WITH THE HUMAN SUPPRESSOR OF FUSED
FILE REFERENCE: 50695-60568
CURRENT APPLICATION NUMBER: US/09/581,831
CURRENT FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: PCT/SE98/02383
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 9704788-0
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 9802293-2
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2239
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS

LOCATION: (167)..(1618)
US-09-581-831-1

Alignment Scores:
Pred. No.: 37.4 Length: 2239
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
DB: 4 Gaps: 0

US-09-315-355C-10 (1-501) x US-09-581-831-1 (1-2239)

Qy 240 LysLysLysLysLysGlyLysLys 248
Db 2213 AAAAAAAAAAAAAAAAAAGAGAAAAA 2239

RESULT 14
US-09-402-532-38
Sequence 38, Application US/09402532
Patent No. 6498019
GENERAL INFORMATION:
APPLICANT: Taniyama, Yoshio
TITLE OF INVENTION: NOVEL PROTEIN, ITS PRODUCTION AND USE
FILE REFERENCE: 2456USOP
CURRENT FILING DATE: 1999-10-04
EARLIER APPLICATION NUMBER: PCT/JP98/01643
EARLIER FILING DATE: 1998-04-09
EARLIER APPLICATION NUMBER: JP 10-010289
EARLIER FILING DATE: 1998-01-22
EARLIER APPLICATION NUMBER: JP 9-184885
EARLIER FILING DATE: 1997-07-10
EARLIER APPLICATION NUMBER: JP 9-093355
EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 43
SOFTWARE:
SEQ ID NO 38
LENGTH: 2867
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Unsure (5' flanking promoter sequence of genomic DNA)

US-09-402-532-38

Alignment Scores:
Pred. No.: 47.5 Length: 2867
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
DB: 4 Gaps: 0

US-09-315-355C-10 (1-501) x US-09-402-532-38 (1-2867)

Qy 240 LysLysLysLysLysGlyLysLys 248
Db 1316 AAAAAAAAAAAAAAAAAAGAGAAA 1342

RESULT 15
US-08-482-918-47/c
Sequence 47, Application US/08482918
Patent No. 6207417
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Bosseiman, Robert A.
APPLICANT: Sug98, Sidney V.
APPLICANT: Martin, Francis H.
TITLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,918
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/33005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 5864 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: join(565..579, 1684..1797, 2693..2755, 3351..3521, 3932..4088, 4314..4397, 4778..4887, 5208..5275, 5677..5713)
LOCATION: 5677..5713)
NAME/KEY: mat_peptide
LOCATION: join(1744..1797, 2693..2755, 3351..3521, 3932..4088, 4314..4397, 4778..4887, 5208..5275, 5677..5713)
LOCATION: ..5713)
US-08-482-918-47

Alignment Scores:
Pred. No.: 95.2 Length: 5864
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.80% Indels: 0
DB: 3 Gaps: 0

US-09-315-355C-10 (1-501) x US-08-482-918-47 (1-5864)

Qy 240 LysLysLysLysLysGlyLysLys 248
Db 5792 AAAAAAAAAAAAAAAAAAGAGAG 5766

Search completed: January 31, 2004, 04:45:08
Job time : 93 secs

THIS PAGE BLANK (USPTO)

Score: 395.00 Matches: 395
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.84% Indels: 0
DB: 12 Gaps: 0

US-09-315-355c-10 (1-501) x US-10-264-049-376 (1-2584)

107 AspaIaIuThrLeuGluGluSerLeuLeuThyValIYrGlySerAsnAspGln 126
131 GATGCTAGAGCTCTTGGAATCTCTCTGGGCTTACGATCTACGGAGAGTAATCA 190
127 AspProTyValThrLeuYAspThrGluGlnTyrgIuArgGluAspPheLeuIlys 146
191 GATCCTTACGTTACTCTGAAAGATACAGAACATATGAACTGAAGATTCTTGATTA 250
147 ProSerAspLeuLeuIleValCysGlyArgAlaGluGlnAspGlnCysAsnLeuGluVal 166
251 CCCAGTGATTAATCTTATGTTGTGGCCGACCTGAAACGACCAAGTGCATTTAGAGGTG 310
167 HisValIYrAsnGlnGluAspSerPheTyValHisHisAspIleLeuLeuSerAla 186
311 CATGTTTATATCAAGAAAGAAAGACTTTTATATGACCAATGATATATCTTGTCTGCA 370
187 TyrProLeuSerValGluTrpLeuAsnPheAspProSerProAspAspSerThrGlyAsn 206
371 TATCCTCTGAGTGGGAATGGCTGATTTTGTCTTACCCAGATGATTTACTGGAAT 430
207 TyrIleAlaValGlyAsnMetThrProValIleGluValITrpaPLeuAspIleValAsp 226
431 TACATTGCTGTAGGAAACATGACCCCTGTTATGAGTGGGACCTTGATATAGTGAC 490
227 SerLeuGluProValPheThrLeuGlySerIysLeuSerIysIysIysValGlyValGly 246
491 TCTTACGCCAGCTTCTACACTCGAGATTAACCTTTAAAGAAAGAAAGAAAGAAAG 550
247 LysIysSerSerSerAlaGluGlyHisThrAspAlaValLeuAspLeuSerTrpAsnIys 266
551 AAGAAGAGTCTCTGACGAAAGGGGATACCGATGCTGCTTGAACCTTTCATGGAATAG 610
267 LeuIleArgAsnValLeuAlaSerAlaSerAlaAspAsnThrValIleLeuTrpAspMet 286
611 CTAATCAGAAATGTTTGAAGAGTGCATCAGTGCACCACTGTAATCTGTGGAGATAG 670
287 SerLeuGlyLysProAlaAlaSerLeuAlaValHisThrAspIysValGlnThrLeuGln 306
671 TCCCTGGGAAACCAAGCAGTACCTCGCTGACACAGACAGAGTCCAAACTGCTGAG 730
307 PheHisProPheGluAlaGlnThrLeuIleSerGlySerTyAspIysSerValAlaLeu 326
731 TTTTATCATTTTGAAGCACAAGCTCTGATTTCTGGCTCATATGATAGTGGCTTGG 790
327 TyrAspCysArgSerProAspGluSerHisArgMetTrpArgPheSerGlyGlnIleGlu 346
791 TATCACTCCCAAGTCCAGATGAAGCCATGCAATGTGGCATTCAGTGGCAGATAGAG 850
347 ArgValITrTrpAsnHisPheSerProCysHisPheLeuAlaSerThrAspAspGlyPhe 366
851 AGAGTACCTTGGAACTCTTTCACCTTGTCACTTGTGGCAGACAGATGACGGCTTT 910
367 ValTyraLeuLeuAspAlaArgSerAspIysProIlePheTrpLeuAsnAlaHisAsnAsp 386
911 GATATATTTTGGATGACGTTTACATAGCCAAATTTTACATTAAGCCACACAATAT 970
387 GluIleSerGlyLeuAspLeuSerSerGlnIleGlyCysLeuValIThrAlaSerAla 406
971 GAAATCTCTGGCTTGATCTTAGCAGTCAATCAAGGCTGCTGTGATGATGCTTCACT 1030
407 AspIysTyValIysIleTrpAspIleLeuGlyAspArgProSerLeuValHisSerArg 426
1031 GACAAATACGTAAGATCTGGACATCTTAGAGATAGCCAAAGTCTAGTTCATTCTAGG 1090
427 AspMetLysMetGlyValLeuPheCysSerSerCysCysProAspLeuProPheIleTyr 446

1091 GACATGAAATGGAGAGTCTCTCTGTTCTCAIGTGGCCCTAATTTGCCATTTATTTAT 1150
447 AlAPheGlyGlyGlnIysGluGlyLeuArgValITrpaPleIleSerThrValSerSerVal 466
1151 GCCTTTGGAGGTCAAAAGAAAGGCTTCCGGCTTGGGATTTAAGACAGACTCTTTCAGTA 1210
467 AsnGluAlaPheGlyArgArgGluArgLeuValLeuGlySerAlaArgAsnSerSerIle 486
1211 AATGAACATTTTGGAAACAGAGAGGCTTGTCTTGTGGAGTGCAGAAATTCATCTATT 1270
487 SerGlyProPheGlySerArgSerSerAspThrProMetGluSer 501
1271 AGTGGCCCTTTTGGCACAGAGCTCAGATACACCAATGAGTCT 1315

RESULT 2

US-10-012-697-1445
Sequence 1445, Application US/10012697
Publication No. US20030215803A1
GENERAL INFORMATION:
APPLICANT: Escobedo, Jaime
APPLICANT: Garcia, Pablo Dominguez
APPLICANT: Kassem, Alfat
APPLICANT: Lamson, George
APPLICANT: Scott, Beth
APPLICANT: Drmanac, Radoje
APPLICANT: Crkvenjakov, Radomir
APPLICANT: Dickson, Mark
APPLICANT: Drmanac, Snezana
APPLICANT: Labat, Ivan
APPLICANT: Leshkowitz, Dena
APPLICANT: Kila, David
APPLICANT: Garcia, Veronica
APPLICANT: Jones, Lee William
APPLICANT: Steche-Crain, Birgit
TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
FILE REFERENCE: 2300-16252
CURRENT APPLICATION NUMBER: US/10/012,697
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: 60/254,648
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 60/275,668
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 1568
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 1445
LENGTH: 1468
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-697-1445

Alignment Scores:

Pred. No.: 1,55e-242 Length: 1468
Score: 253.00 Matches: 253
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.50% Indels: 0
DB: 13 Gaps: 0

US-09-315-355c-10 (1-501) x US-10-012-697-1445 (1-1468)

249 SerSerSerAlaGluGlyHisThrAspAlaValLeuAspLeuSerTrpAsnIysLeuIle 268
707 AGTTCCTCAGAGAAAGGCATACCGATGCTGCTTACCTTTCATGGAATAGCTAATC 766
269 ArgAsnValLeuAlaSerAlaSerAlaAspAsnThrValIleLeuTrpAspMetSerLeu 288
767 AGAATGTTTITTAAGCAATGCAATCAGTGCACACACTGTAATTCGTGGATATGCTCTG 826
289 GlyLysProAlaAlaSerLeuAlaValHisThrAspIysValGlnThrLeuGlnPheHis 308
827 GGGAAACAGAGAGCTACCTGCTGTACACACAGACAAGGTCCAAACACTGCACTTTCAT 886

```
QY 309 ProPheGluAaGlnThrIleuIleSerGlySerTyrAspIleValAlaIleuTyrAsp 328
Db 887 CCAATTTAGAGACAGACCTGATTTCTGGCATATATAGTACAGTGGCTTTATGAC 946
QY 329 CysArgSerProAspGluSerHisArgMetThrArgPheSerGlyGlnIleGluArgVal 348
Db 947 TGCAGAGTCCAGATGGAAGCCATGCAATGTGGGATTCAGTGGCAGATGAGAGAGTG 1006
QY 349 ThrTrpAsnHisPheSerProCysHisPheIleuIleSerThrAspAspGlyPheValTyr 368
Db 1007 ACTTGAATCACTTTTACCTTGATATTTCTTGCCAGTACAGATGACGGCTTTGATAT 1066
QY 369 AsnIleuAspAlaArgSerAspIleProIlePheThrIleuAsnAlaHisAsnAspGluIle 388
Db 1067 AATTGGATGACGCTTGCAGTAAGCCAAATTTTACACTTAATGACACCAATGAGAAATC 1126
QY 389 SerGlyIleuAspIleuSerSerGlnIleGlyCysIleuValThrAlaSerAlaAspIys 408
Db 1127 TCTGTCTTGATCTTACGACATCAATCAAGGCTGTCTCGACTGCTTCAGTGCAGACAA 1186
QY 409 TyrAlaIysIleTProAspIleuGlyAspArgProSerIleuValHisSerArgAspMet 428
Db 1187 TACGTGAAGATCTGGACATCTTAGAGATAGGCCAAGTCAATTCATTAGAGGACATG 1246
QY 429 LysMetGlyValIleuPheCysSerSerCysCysProAspIleuProPheIleTyrAlaPhe 448
Db 1247 AAAATGGAGATCTCTCTGTTCTTCAATGTTGCCCTGATTTGCCATTTATTTAGCCTT 1306
QY 449 GlyGlyGlnIysGluGlyIleuArgValTyrAspIleSerThrValSerSerValAsnGlu 468
Db 1307 GGAGGTCAAAAAGAGGCTTCGGGCTCGGATTAAGCAACAGCTCTTCAGTAAATGAA 1366
QY 469 AlaPheGlyArgArgGluArgIleuValIleuGlySerIleArgAsnSerSerIleSerGly 488
Db 1367 GCATTTGGAACAGACGAGGCTTGTCTTGGAGTGCAAGAAATTCATCTATTAGTGC 1426
QY 489 ProPheGlySerArgSerSerAspThrProMetGluSer 501
Db 1427 CCTTTGGCAGCAGAGCTCAGATACACCCATGAGTCT 1465

RESULT 3
US-10-242-535A-9829
; Sequence 9829, Application US/10242535A
; Publication No. US2004001363A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9829
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (38)..(38)
```

```
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-9829
Alignment Scores:
Pred. No.: 2 66e-93 Length: 400
Score: 103.00 Matches: 103
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 20.56% Indels: 0
DB: 12 Gaps: 0

US-09-315-355C-10 (1-501) x US-10-242-535A-9829 (1-400)
QY 399 GlyCysIleuValThrAlaSerAlaAspIleTyrValIysIleTyrAspIleIleuGlyAsp 418
Db 76 GCGCTGTCTGAGACTGCTTACGCTGACCAATAGCTGAAGATCTGGACATCTTAGAGAT 135
QY 419 ArgProSerIleuValHisSerArgAspMetLysMetGlyValIleuPheCysSerSerCys 438
Db 136 AGGCCAAGTCTAGTTCATTCTAGGACATGAAATGGAGATTCTCTGTTCTTCATGT 195
QY 439 CysProAspIleuProPheIleTyrAlaPheGlyGlyGlnIysGluIleuArgValTyr 458
Db 196 TGCCCTAATTTGCCATTTATTTATGCTTTGGAGGTCAAAAAGAGGCTTCGGGCTGG 255
QY 459 AspIleSerThrValSerSerValAsnGluAlaPheGlyArgArgGluArgIleuValIleu 478
Db 256 GATTAAGCACAGCTCTTTCAGTAATGAAGCATTGGAAGACGAGAGAGCTTGTCTT 315
QY 479 GlySerAlaArgAsnSerSerIleSerGlyProPheGlySerArgSerAspThrPro 498
Db 316 GGGAGTCAAGAAATTCATCTATTAGTGCCCTTTTGGCAGCAGAGACTCAGATACACC 375
QY 499 MetGluSer 501
Db 376 ATGAGTCT 384

RESULT 4
US-10-242-535A-16383
; Sequence 16383, Application US/10242535A
; Publication No. US2004001363A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16383
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Human
; US-10-242-535A-16383
Alignment Scores:
Pred. No.: 3 35e-72 Length: 568
Score: 82.00 Matches: 82
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.37% Indels: 0
DB: 12 Gaps: 0

US-09-315-355C-10 (1-501) x US-10-242-535A-16383 (1-568)
```

QY 302 ValGlnThrLeuGlnPheHisProPheGluValGlnThrLeuIleSerGlySerTyrAsp 321
Db 171 GTCCAAACACTGCAGCTTTCATCCATTTGACACAGACTGATTTCTGGCTCATATGAT 230
QY 322 LysSerValAlaLeuTyrAspCysArgSerProAspGluSerHisArgMetTyrAspPhe 341
Db 231 AAGTCAGGCTTTGTATGATGATGCGGAAGTCAGATGAAAGCCATGCAATGTGGCGGATTC 290
QY 342 SerGlyGlnIleGluArgValThrTyrAsnHisPheSerProCysHisPheLeuAlaSer 361
Db 291 AGTGGCAGATAGAGAGAGTACTGATGATCTTTCACCTTGTCATTTCTTGGCCAGT 350
QY 362 ThrAspAspGlyPheValTyrAsnLeuAspAlaArgSerAspIlePheThrLeu 381
Db 351 ACAATGACGCGCTTGTATATATTTGATGATGATGATGATGATGATGATGATGATGATGAT 410
QY 382 AsnAla 383
Db 411 AATGCC 416

RESULT 5

US-09-916-995-21467
; Sequence 21467, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918, 995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235, 076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq For Windows Version 3.0
; SEQ ID NO 21467
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ... (508)
; OTHER INFORMATION: n = A, T, C or G
US-09-918-995-21467

Alignment Scores:

Pred. No.: 2,92e-62 Length: 508
Score: 72.00 Matches: 72
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 14.37% Indels: 0
DB: 11 Gaps: 0

US-09-315-355C-10 (1-501) x US-09-918-995-21467 (1-508)

QY 430 MetGlyValLeuPheCysSerSerCysCysProAspLeuProPheIleTyrAlaPheGly 449
Db 61 ATGGAGATTCCTCTTCTGTTCTTCAGTTCAGCCCTGATTTGATTTATGATGATGATGATGAT 120
QY 450 GlyGlnIleGlyGluLeuArgValTyrAspIleSerThrValSerSerValAsnGluAla 469
Db 121 GGTCAAAAGAGAGAGGCTTGGGCTGCGATTAAGCAGAGCTCTTCACTGAATGAAGCA 180
QY 470 PheGlyArgArgGluArgLeuValLeuGlySerAlaArgAsnSerSerIleSerGlyPro 489
Db 181 TTGGAAGAGCAGAGAGGCTTGTCTTGGGAGTGCAGAAATTCATCTATTAGTGGCCCT 240
QY 490 PheGlySerArgSerSerAspThrProMetGluSer 501
Db 241 TTGGCAGCAGAGCTCAGATACCCCATGAGATCT 276

RESULT 6

US-10-062-674-1561
; Sequence 1561, Application US/10062674
; Publication No. US20040005559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062, 674
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: US 09/625,102
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 1561
; LENGTH: 3024
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040005559A1 124921.6
; LOCATION: (1) ... (3024)
; OTHER INFORMATION: a, t, c, g, or other
US-10-062-674-1561

Alignment Scores:

Pred. No.: 1,44e-60 Length: 3024
Score: 71.00 Matches: 97
Percent Similarity: 97.98% Conservative: 0
Best Local Similarity: 97.98% Mismatches: 0
Query Match: 14.17% Indels: 2
DB: 12 Gaps: 0

US-09-315-355C-10 (1-501) x US-10-062-674-1561 (1-3024)

QY 337 ArgMetTyrArgPheSerGlyGlnIleGluArgValThrTyrAsnHisPheSerProCys 356
Db 1211 CGAATGGCGGATTCAGTGCAGATGAGAGAGTGCATTTGATCCTTTCATCCTTGT 1270
QY 357 HisPheLeuAlaSerThrAspAsp-GlyPheValTyrAsnLeuAspAlaArgSerAsp 376
Db 1271 CATTCTTGCCAGTCAGATGAGAGCGGCTTGTATATATTTGATGATGATGATGATGATGAT 1330
QY 376 sProIlePheThrLeuAsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSerSerG 396
Db 1331 GCCAATTTTACACTTATATGACACAAATGATGAAATCTGCTGATCTTATGACATCA 1390
QY 396 nIle-LysGlyCysLeuValThrAlaSerAlaAspLysTyrValLysIleTyrAspIle 416
Db 1391 AATCCAAAGGCTGCTGTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 1450
QY 416 euGlyAspArgProSerLeuValHisSerArgAspMetLysMetGlyValLeu 433
Db 1451 TAGAGATAGAGCCAAAGCTGATTCATTTAGGAGCAATGAAATGGAGTTCTC 1503

RESULT 7

US-10-029-386-9515
; Sequence 9515, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Penn, Sharon G.
; APPLICANT: Penn, Sharon G.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 9515
; LENGTH: 539


```
;; PRIOR APPLICATION NUMBER: US 09/625,102
;; PRIOR FILING DATE: 2000-07-24
;; NUMBER OF SEQ ID NOS: 2217
;; SOFTWARE: PERL Program
;; SEQ ID NO 1082
;; LENGTH: 313
;; TYPE: DNA
;; ORGANISM: Mus musculus
;; FEATURE:
;; NAME/KEY: misc feature
;; OTHER INFORMATION: GenBank ID No. US2004005559A1 g1677315
US-10-062-674-1082

Alignment Scores:
Pred. No.: 1,71e-36 Length: 313
Score: 46.00 Matches: 46
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.18% Indels: 0
DB: 12 Gaps: 0

US-09-315-355c-10 (1-501) x US-10-062-674-1082 (1-313)

Qy 221 Aspleuasp11eValaspSerLeuGluProValpHeThLeuGlySerLyLeuSerLyS 240
Db 3 GACCTGGATATAGTGAAGCTCTCTGAAACCACTCTTCACTGGAGCAAGCTTCCAAA 62

Qy 241 LybalySlySlySlySlySlySlySlySlySlySlySlySlySlySlySlySlySly 260
Db 63 AAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 122

Qy 261 AspleuSerTPanLyS 266
Db 123 GACCTATCTCGAATTAAG 140

RESULT 11.
US-10-012-697-413/C
;; Sequence 413, Application US/10012697
;; Publication No. US20030215803A1
;; GENERAL INFORMATION:
;; APPLICANT: Escobedo, Jaime
;; APPLICANT: Garcia, Pablo Dominguez
;; APPLICANT: Kaasam, Altaf
;; APPLICANT: Lamson, George
;; APPLICANT: Scott, Beth
;; APPLICANT: Drmanac, Radoje
;; APPLICANT: Cirvenjakov, Radomir
;; APPLICANT: Dickson, Mark
;; APPLICANT: Drmanac, Snezana
;; APPLICANT: Labat, Ivan
;; APPLICANT: Leeshkowitz, Dena
;; APPLICANT: Kita, David
;; APPLICANT: Garcia, Veronica
;; APPLICANT: Jones, Lee William
;; APPLICANT: Steche-Crain, Birgit
;; TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
;; TITLE OF INVENTION: ISOLATED FROM HUMAN PROSTATE
;; FILE REFERENCE: 2300-16252
;; CURRENT APPLICATION NUMBER: US/10/012,697
;; CURRENT FILING DATE: 2003-01-21
;; PRIOR APPLICATION NUMBER: 60/1254,648
;; PRIOR FILING DATE: 2000-12-07
;; PRIOR APPLICATION NUMBER: 60/275,668
;; PRIOR FILING DATE: 2001-03-13
;; NUMBER OF SEQ ID NOS: 1568
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 413
;; LENGTH: 667
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1, 3, 10, 12, 434, 452, 457, 575, 589, 611, 615, 633, 640,
;; NAME/KEY: misc feature
```

```
;; LOCATION: 663
;; OTHER INFORMATION: n = A,T,C or G
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1, 3, 10, 12, 434, 452, 457, 575, 589, 611, 615, 633, 640,
;; LOCATION: 663
;; OTHER INFORMATION: n = A,T,C or G
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1, 3, 10, 12, 434, 452, 457, 575, 589, 611, 615, 633, 640,
;; LOCATION: 663
;; OTHER INFORMATION: n = A,T,C or G
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: 1, 3, 10, 12, 434, 452, 457, 575, 589, 611, 615, 633, 640,
;; LOCATION: 663
;; OTHER INFORMATION: n = A,T,C or G
US-10-012-697-413

Alignment Scores:
Pred. No.: 3.27e-29 Length: 667
Score: 39.00 Matches: 39
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.78% Indels: 0
DB: 13 Gaps: 0

US-09-315-355c-10 (1-501) x US-10-012-697-413 (1-667)

Qy 168 ValTyRanGlnGluGluAspSerPheTyRValHisAspIleLeuSerAlaTyR 187
Db 244 GTTATATATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATAT 185

Qy 188 ProLeuSerValGluTrpLeuAnpHeAspProSerProAspAspSerThrgLyAsn 206
Db 184 CCTGTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATAT 128

RESULT 12.
US-10-242-535A-57161
;; Sequence 57161, Application US/10242535A
;; Publication No. US20040013663A1
;; GENERAL INFORMATION:
;; APPLICANT: ChondroGene Inc.
;; APPLICANT: Liew, C.C.
;; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
;; FILE REFERENCE: 4231/2005
;; CURRENT APPLICATION NUMBER: US/10/242,535A
;; CURRENT FILING DATE: 2002-09-12
;; PRIOR APPLICATION NUMBER: US 10/085,783
;; PRIOR FILING DATE: 2002-02-28
;; PRIOR APPLICATION NUMBER: US 60/305,340
;; PRIOR FILING DATE: 2001-07-13
;; PRIOR APPLICATION NUMBER: US 60/275,017
;; PRIOR FILING DATE: 2001-03-12
;; PRIOR APPLICATION NUMBER: US 60/271,955
;; PRIOR FILING DATE: 2001-02-28
;; NUMBER OF SEQ ID NOS: 58994
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 57161
;; LENGTH: 222
;; TYPE: DNA
;; ORGANISM: Human
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (24)-(24)
;; OTHER INFORMATION: n is a, c, g, or t
;; NAME/KEY: misc_feature
```



```

; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 1168
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-1168
    
```

```

Alignment Scores:
Pred. No.:      0.0217      Length:      476
Score:          12.00      Matches:      12
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      2.40%      Indels:      0
DB:               10      Gaps:      0
    
```

US-09-315-355c-10 (1-501) x US-09-998-598-1168 (1-476)

```

QY      240 LysLysLysLysLysLysGlyLysLysSerSerSer 251
          |||||
Db       75 AAAAAAAAAAAAAAAAAAGGAAAAAAAAAGCAGCTCT 40
    
```

Search completed: January 31, 2004, 06:02:16
 Job time : 510 secs


```

CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: 60/254,648
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 60/275,668
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 1568
SOFTWARE: FASTSQ for Windows Version 4.0
SEQ ID NO 1445
LENGTH: 1468
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-697-1445

Alignment Scores:
Stred. No.:      2.2e-297
Score:           2547.50
Percent Similarity: 97.21%
Best Local Similarity: 97.21%
Query Match:     96.50%
DB:              13
Gaps:

```

US-09-315-355C-10 (1-501) x US-10-012-697-1445 (1-1468)

Qy	1	MetAspHisSerArgGlnValThrCysValAlaIleProValArgCysGluValAlaValSerGlu	20
Db	1	ATGAACCGCAGCCGACAGGTGACGTGCGGCTGAGTCCGTGGGGGTGGCCAAAGAG	60
Qy	21	ThrProAspIysValGlnIleuSerIysGluGluValIysArgLeuIleAlaGluAlaLys	40
Db	61	ACACCGACAAAGGTAAAGCTGAGTAAAGAAAGATTAACCCCTCATTTGCTGAGCGAAG	120
Qy	41	GluIysLeuGlnGlnGlnGlyGlyIysAspGlnGlnGlnThrGlyIserProSerGlu	60
Db	121	GAGAAATTGCAGAGAGAGGTGGTGGCATTGATGAAGAGAGAGACAGGACGCTTTCAGAA	180
Qy	61	AspGlyMetGlnSerAlaArgThrGlnAlaArgProArgGluProLeuGlnAspGlyAsp	80
Db	181	GATGGCATGTGACAGTCCAGCACCCAGGACCCCAAGAGGCCCTTGAGAGATGGTAC	240
Qy	81	ProGlnAspAspArgThrLeuAspAspAspGlnLeuAlaGluTyrAspLeuAspIysTyr	100
Db	241	CCAGAGATACAGGACGCTGTATGATGTATGAGCTGGCTGGATGACATTGAATAATAT	300
Qy	101	AspGlnGlnGlyAspProAspAlaGluThrLeuGlnGlyIserLeuGlnIleuThrVal	120
Db	301	GATGAGGAAGGTAAACCAATGCTGAGACTCTTGGTGAATCTCTTGGCTTTACGGTC	360
Qy	121	TyrGlySerAsnAspGlnAspProTyrValThrLeuLysAspThrGlnGlnTyrGluArg	140
Db	361	TACGGGAGTATGATCAAGATCTTACGTTACTCGAAGAATACGAACATATGAACGT	420
Qy	141	GlnAspPheIleuIleIysProSerAspAsnLeuIleValCysGlyArgAlaGlnGlnAsp	160
Db	421	GAAGATTTCTTGATTAAGCCCAAGCTGATATCTTAATAGTTGGGCCGAGCAACAGAC	480
Qy	161	GlnCysAsnLeuGlnValHisValTyrAsnGlnGlnGlnAspSerPheTyrValHisHis	180
Db	481	CAGTGCATTTAGAGGTGACATGTTATATCAAGAAAGAACCTCTTTTAGTACACCAT	540
Qy	181	AspIleIeuIeuSerAlaTyrProIeuSerValGluTyrPleuAsnPheAspProSerPro	200
Db	541	GATTACTCTTGCTGTCATATCTCTCGAATGCGAAATGGCTGAATTTGATACCTAGCCA	600
Qy	201	AspAspSerThrGlyAsnTyrIleAlaValAlaGlyAsnMetThrProValIleGluValTyr	220
Db	601	GATGATTCTACTGGAATTAACAATGCTGTAGGAACAATGACCCCTGATTATGAAGTGG	660
Qy	221	AspLeuAspIleValIaspSerLeuGluProValPheThrLeuGlySerIlysIeuSerLys	240
Db	661	GACCTTGATATGACACTTCTTAGAGCAGACTTCACACTCGGAAGT-----	709
Qy	240	SlySlySlySlySlyGlyLysLysSerSerSerAlaGlnGlnHisThrAspAlaValLe	260

```

Db      710 -----TCTCAGCAGAAAGGCGATACCGATGCTGCTCT 741
QY      260 uAspLeuSerTrpAsnIysLeuIleArgAsnValLeuAlaSerAlaSerAlaAspAsnTh 280
Db      742 TGACCTTTCAGAGATAGATAGCTTAATCAGAAAGTTTGTGCAAGTGCATCATGCTGCACAAAC 801
QY      280 rValIleLeuTrpAspMetSerLeuGlyLysProAlaAlaSerLeuAlaValHisThAs 300
Db      802 TGTATTCTGTGGGATATGTCTCTTGGGAAACAGACGCTAGCTCGGTGACACACGA 861
QY      300 pLysValGlnThrLeuGlnPheHisProPheGluAlaGlnThrLeuIleSerGlySerTy 320
Db      862 CAAGCTCCAAACATGCGAGCTTTCATCATTTGAGACACAGACTGATTTTCTGGCTCATA 921
QY      320 rAspLysSerValAlaLeuTyraAspCyAArgSerProAspGluSerHisArgMetTrpAr 340
Db      922 TGAATAGCAAGATGGCTTTGTATGTAGCTGCCGAAGTCAGATGAAGCCATCGAATGTGGCG 981
QY      340 gPheSerGlyGlnIleGluArgValIThrTrpAsnHisPheSerProCysHisPheLeuAl 360
Db      982 ATTCAGTGGCGAGATAGAGAGAGGACTTGGAAATCATCTTTCACCTTGTCTCTTCTGGC 1041
QY      360 aSerThrAspAspGlyPheValTyraAsnLeuAspAlaArgSerAspLysProIlePheTh 380
Db      1042 CAGTACAGATACGCGCTTGTATATTAATTGTGATGCAAGCTTCAGATTAAGCCAAATTTTAC 1101
QY      380 rLeuAsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSerSerGlnIleLysGlyCy 400
Db      1102 ACTTAATGCAACACATGATGTAAATCTGTGCTTGATCTTACGATCCAAATCAAGGCGTG 1161
QY      400 sLeuValIThrIaSerAlaAspLysTyraValLysAlaTrpAspIleLeuGlyAspArgPr 420
Db      1162 TCTGTGATCTCTTCAGCTGACAAATACGTGAAGATCTGGACATCTTAGAGATAGGCC 1221
QY      420 oSerLeuValHisSerArgAspMetLysMetGlyValLeuPheCysSerSerCysArgPr 440
Db      1222 AAGCTAGTATTCTTACGGGACATGAATAATGGAGTCTCTTCTGTCTTCATGTTGCC 1281
QY      440 cAspLeuProPheIleTyraIleGlyGlyGlnLysGlyGlyLeuArgValITrpAspI 460
Db      1282 TGATTTGGCATTTTATTTATGCTTTGGAGGCTCAAAAAGAGGCGTCCGGTCTGGGATAT 1341
QY      460 eSerThrValSerSerValaAsnGluAlaPheGlyArgArgGluArgLeuValLeuGlySe 480
Db      1342 AAGACAGCTCTCTTCAGTAAATGAAGCATTTGGAAGACGAAGAGGCTTGTCTTGGAG 1401
QY      480 rAlaArgAsnSerSerIleSerGlyProPheGlySerArgSerSerAspThrPrometG 500
Db      1402 TGCAAGAAATTCATCTATTAGTGGCCCTTTTGGCAGACGAGAGCTCAGATTACCCATG 1461
QY      500 uSer 501
Db      1462 GTCT 1465

RESULT 2
US-10-264-049-376
; Sequence 376, Application US/10264049
; Publication No. US2004000579A1
; GENERAL INFORMATION:
; APPLICANT: Birst et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264, 049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 376
; LENGTH: 2584
; TYPE: DNA

```

ORGANISM: Homo sapiens
US-10-264-049-376

Alignment Scores:

Pred. No.:	5,93e-241	Length:	2584
Score:	2084.00	Matches:	395
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	78.94%	Indels:	0
	12	Gaps:	0

US-09-315-355c-10 (1-501) x US-10-264-049-376 (1-2584)

```

Qy 107 AspAlaGluThrLeuGluSerLeuLeuGlyLeuThrValTyrGlySerAspAla 126
Db 131 GAGGCTAGACTCTTGCTGATCTCTTGGCTTACGGCTACCGGATATGATCA 130
Qy 127 AspProTyrValThrLeuLysAspThrGluGlnTyrGluArgGluAspPheLeu 146
Db 191 GATCCTTACGTTACTCGAAAGATACGAAACAATATACGATGAGATTTCTTGATTA 250
Qy 147 ProSerAspMetLeuLeuValCysGlyArgAlaGluGlnAspGlnCysAsnLeuGluVal 166
Db 251 CCCAGTATATATCTTATAGTTGTGGCCGAGCTGAAACAGACAGTCAATTTAGAGTG 310
Qy 167 HisValTyrAsnGlnGluGluAspSerPheTyrValHisHisAspIleLeuLeuSerAla 186
Db 311 CAGTTTATATATACAGAAAGAAAGACTTTTATGCTACACCATATATACTCTTGCA 370
Qy 187 TyrProLeuSerValGluTyrPleuAsnPheAspProSerProAspAspSerThrGlyAsn 206
Db 371 TATCCTTGAGTGGAGTGGCTGAATTTGATCTTACCCAGATGATTCATCGAAT 430
Qy 207 TyrIleAlaValGlyAsnMetThrProValIleGluValTyrPheLeuAspIleValAsp 226
Db 431 TACATGCTGTAGAAACATGACCCCTGTTATGAAAGTGGGACCTGATATAGTGAC 490
Qy 227 SerLeuGluProValPheThrLeuGlySerLysLeuSerLysLysLysLysGly 246
Db 491 TCTTTAGGCCAGCTTCACTGCACTGGAAAGTAACTTTCAAAAAGAAAGAAAGCA 550
Qy 247 LysLysSerSerSerAlaGluGlyHisThrAspAlaValLeuAspLeuSerTyrAsnLys 266
Db 551 AAGAAAGGTTCTCTCAGCAGAAAGGCAATACGATCTGCTGACCTTTCATGGAATAG 610
Qy 267 LeuIleArgAsnValIleAlaSerAlaSerAlaAspAsnThrValIleLeuTyrAspMet 286
Db 611 CTATTCAGAAATGTTTATAGCAAGTGCATCAGCTCAACAACCTGTAATTCGTGGATATG 670
Qy 287 SerLeuGlyLysProAlaAlaSerLeuAlaValHisThrAspLysValGlnThrLeuGln 306
Db 671 TCTTGGGAAACAGCAGCTGAGCTGCTGTACACAGCAAGGCTCCAAACCTCAG 730
Qy 307 PheHisProPheGluAlaGlnThrLeuIleSerGlySerTyrAspLysSerValAlaLeu 326
Db 731 TTTTATCATTTTGAAGCAGACACTGATTTCTGGCTCATATGATAGTAGTGCTTGG 790
Qy 327 TyrAspCysArgSerProAspGluSerHisArgMetTyrPheSerGlyGlnIleGlu 346
Db 791 TATACCTGCCCAAGTCCAGATGAAGACCATGAAATGAGCATTCAGTGGCCAGATAGAG 850
Qy 347 ArgValThrTyrAsnHisPheSerProCysHisPheLeuAlaSerThrAspAspGlyPhe 366
Db 851 AGAGTGAAGTGAATACACTTTTCACTTGTATTTCTTGCCCATACATGATGAGGCTTT 910
Qy 367 ValTyrAsnLeuAspAlaArgSerAspLysProIlePheThrLeuAsnAlaHisAsnAsp 386
Db 911 GTATATATATTTGATGACAGCTTCAGATAGCCAAATTTTACACTTAATGCAACAATGAT 970
Qy 387 GluIleSerGlyLeuAspLeuSerSerGlnIleLysGlyCysLeuValThrAlaSerAla 406
Db 971 GAAATCTCTGCTTGATCTTACAGATCAAAATCAAGGGCTGTCTGTGATGCTTCAAGCT 1030

```

```

Qy 407 AspLysTyrValLysIleThrAspIleLeuGlyAspArgProSerLeuValHisSerArg 426
Db 1031 GACAAATACGTAAAGATCTGGAGACATCTTAGAGATAGGCCAAGCTTACTTCACTTAG 1090
Qy 427 AspMetLysMetGlyValLeuPheCysSerSerCysCysProAspLeuProPheIleTyr 446
Db 1091 GACATATAAATGGAGATCTCTTCTGTTCTTCAATGTTGCCCTGATTTGCCATTTATAT 1150
Qy 447 AlaPheGlyGlyGlnLysGluGlyLeuArgValTyrAspIleSerThrValSerSerVal 466
Db 1151 GCCTTGGAGGTCAAAAAGAGGGCTTGGCTGCGATATAGCACACTCTTTCAGTA 1210
Qy 467 AsnGluAlaPheGlyArgArgGluArgLeuValLeuGlySerAlaArgAsnSerIle 486
Db 1211 AATGAAGCAATTTGAAGACGAGAGAGCTTGTCTTGGAGTGCAGAAATTCATCTATT 1270
Qy 487 SerGlyProPheGlySerArgSerSerAspThrProMetGluSer 501
Db 1271 AGTGGCCCTTTTGGCAGCAGAGCTCAGATACACCATGAGTCT 1315

RESULT 3
US-10-062-674-1561
; Sequence 1561, Application US/10062674
; Publication No. US20040005559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062,674
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: US 09/625,102
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 1561
; LENGTH: 3024
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040005559A1 124921.6
; FEATUDB:
; NAME/KEY: unsure
; LOCATION: (1) ... (3024)
; OTHER INFORMATION: a, t, c, g, or other
US-10-062-674-1561

Alignment Scores:
Pred. No.: 1,31e-201 Length: 3024
Score: 1759.50 Matches: 429
Percent Similarity: 81.64% Conservative: 20
Best Local Similarity: 78.00% Mismatches: 49
Query Match: 66.65% Indels: 53
DB: 12 Gaps: 9

US-09-315-355c-10 (1-501) x US-10-062-674-1561 (1-3024)
Qy 4 SerArgGlnValThrCysVal---AlaTyr-ValArgCysGlyValAlaLysGluThrPr 22
Db 131 GCCCGCCAAATGATTCGTGGTAGGCTGAGTCCCTGGGGGTGCCAAAGACACC 190
Qy 22 aaPlyValGluLeuSerLysGluGluValLysArgLeuIle-AlaGluAlaLysGlu 42
Db 191 AGCAAGGTAGAGCTAGTAAAGAAAGTAAAGCTCAATCTGCTGAGGCAAGAGAG 250
Qy 42 LysLeuGlnGluGluGlyGlySerAspGluGluGlnThrGlySerProSerGluAsp 62
Db 251 AATTGAGAGAAAGGTGGTGGATGATGAAGAGACAGCACTTTCAGAAAGATG 310
Qy 62 LysMetGln-----SerAlaArgThrGlnAlaArgProArgGluProL 76
Db 311 GCATGAGATGTGCCAGCGCCAGCCCACTGCGCCCCCAATGATGTAAGCCCCCTG 370

```

```

Qy 76 euGluaSp-GlyAspPro-GluAspAspArgThrLeuAsp-AspAspGluLeuAlaGluT 95
Db 371 TGAAGCATGTGTGACCCATGAGATGACAGACCGCTTGTAATATGAGCTGCTGAGT 430
Qy 95 YrAspLeuAspLysThrAspGluGluGluYrAspProAspAlaGluThrLeuGly----- 112
Db 431 ACGACTAGATAATATGATGAGAGAGGTGACCCAGATGCTGAACACTCTGGCTGAGATC 490
Qy 113 -----GluSerLeuLeuGlyLeuThrValTyrGlySerAsnAspGlnAspProTyr--V 130
Db 491 TCTCTTAGGCTCTTAACGGGCTTAACGGGGAATATAGTCAAGAGACTCTTAGCT 550
Qy 130 alThrLeuYrAspThrGluGlnTyrGluArgGluAspPheLeuIleLysProSerAsp 150
Db 551 TACTTCGAAAGATACAGAACATATGAACTGAAGATTTCTTATTAAGCCCGTAT 610
Qy 150 sn-LeuIleValCysGlyArgAlaGluGlnAspGlnCysAsnLeuGluValIleValTyr 169
Db 611 ATTCTTATAGTTGTGGCCGAGCTGAACAGACAGCAATTTAAGAGTGCATGTTAT 670
Qy 170 AsnGlnGluGlu-AspSerPheTyrValIleHisAspIleLeuLeuSerAlaTyrProLe 189
Db 671 AATCCAGAAAGAAAGACTTTTATGACACCAAGATATCTCTTGCTGATTCCTCT 730
Qy 189 uSerValGluTyrLeuAsnPheAspProSerProAspAspSerThr-GlyAsnTyrIleA 209
Db 731 GAGGTGGATGGCTGATTTGATTCACGCCAGATGATTTCTAGGAAATTAACAT 790
Qy 209 laVal-GlyAsnMetThrProValIleGluValTyrAspLeuAspIle-Val----- 225
Db 791 CTGTAGGAAACATGACCCCTGTATGAACTGTGGACCTGTGAATATTAAAGGGGTT 850
Qy 226 -----AspSerLeuGluProValPheThrLeu-GlySerLysLeuSerLysLysL 242
Db 851 TTGGGGGGGGGACCTTTAGACCAAGCTTTCACCTGGGGAAGTAACTTTCAAAAAAGA 910
Qy 242 YrLysLysLysGlyLysLysSerSerSerAlaGluGlyHisThrAspAlaVal-LeuAsp 261
Db 911 AGAAAAAGAAAGAAAGAGTTCTCTCAGCAAGAGGCATACCGATGCTGCTCGT 970
Qy 262 LeuSerTyr-AsnLysLeuIleArgAsnValLeu--AlaSerAlaSerAla-AspAsn 280
Db 971 CTTCATGAGGAATAGCTAATTCGCAGAAATGTTTAAAGCAAGTCATCAGCTGACACA 1030
Qy 280 hrValIleLeuTyrAspMetSer-LeuGlyLysPro-AlaAlaSerLeuAlaValIleSt 299
Db 1031 CTGTAAATTCGTGGATATGTCCTTGAGAACACAGACACTGAGCTCGTACAC 1090
Qy 299 rAspLysValGlnThrLeuGlnPheHisProPheGluAlaGlnThrLeuIleSer-Glys 319
Db 1091 AGACAAAGGTCCAAACATGCACTTTCATTCATTTGAAGCACAGACTGATTTCTGGGCT 1150
Qy 319 erTyrAspLysSerValAlaLeu--TyrAspCysArgSerProAsp--GluSerHis- 336
Db 1151 CATATGATTAAGTCTAGTGGCTTTGTATTTGACTCCGAGAGCCAGATTGAAAGCCATC 1210
Qy 337 ArgMetTyrAspPheSerGlyGlnIleGluArgValThrTyrPheHisAspSerProCys 356
Db 1211 CGAATGTGGCCATTCAGTGGCAGATGAGAGAGTGTGAGTCACTTTCACTTCTGT 1270
Qy 357 HisPheLeuAlaSerThrAspAsp-GlyPheValTyrAsnLeuAspAlaArgSerAspLys 376
Db 1271 CATTTCTTGCCAGTACAGATGACGGGCTTTGTATATATTTGATGACACTTACAGTAA 1330
Qy 376 spPheIlePheThrLeuAsnAlaHisAsnAspGlnIleSerGlyLeuAspLeuSerSerG 396
Db 1331 GCCAATTTTTCACCTTAATGACACCAATGATGAATCTCTGCTTATCTTACACTCA 1390
Qy 396 nIle-LysGlyCysLeuValThrAlaSerAlaAspLysTyrValLysIleTyrAspIleL 416
Db 1391 AATCAAGGGCTGTCTGTGCTCTTCACTGCAAAATAGTGAAGATCTGGGAAACATCT 1450
Qy 416 euGlyAspArgProSerLeuValHisSerArgAspMetLysMetGlyValLeuPhe-Cys 435

```

```

Db 1451 TAGAGATAGCCCAAGCTCATTGATGAGGACATGAAAGGAGGAGTCTGCTGT 1510
Qy 436 SerSerCysCysProAspLeuPro----PheIleTyrAlaPheGlyGlyGlnLysGly 454
Db 1511 GTGCAATGTGCTGAGTCCAGCTTTCATTTATGATGTGTTGCA-GGTCAAAAGAAAGG 1569
Qy 455 LeuArgValTyr-AspIleSerThrValSerSerValAsn--GluAlaPheGlyArgAr 473
Db 1570 CTTCGGGCTGGGAGATATAGACACAGCTCTTCAGAAATGAGACATTTGGAAGACG 1629
Qy 473 gGlu-ArgLeuValLeuGlySer-AlaArgAsnSerSer-IleSerGlyProPheGlyS 492
Db 1630 AGAGAGGCTGTGCTTGTGGGACCTGCAAGAAATTCATTTATTCAGTGGCCCTTTGGCA 1689
Qy 492 erArgSerAspThr-PrometGluSer 501
Db 1690 GCAGAGCTCAGATACCCCAATGAGTCC 1719

```

RESULT 4

```

US-10-128-714-2208
; Sequence 2208, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Weng
; APPLICANT: Rishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Broshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128, 714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2208
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-2208

```

Alignment Scores:

```

Pred. No.: 2,08e-102 Length: 1620
Score: 935.50 Matches: 207
Percent Similarity: 56.73% Conservative: 88
Best Local Similarity: 39.81% Mismatches: 196
Query Match: 35.44% Indels: 29
DB: 15 Gaps: 10

```

US-09-315-355c-10 (1-501) x US-10-128-714-2208 (1-1620)

```

Qy 4 SerArgGlnValThrCysValAlaTyrPValArgCysGlyValAlaLysGluThrProAsp 23
Db 4 TCTTATAGATGCTCACTGACCGCTTGCGGCGGAGAGTCCCTCCCAATTCCTACC 63
Qy 24 YrValGluLeuSerLysGluGluValLysArgLeuIleAlaGluAlaLysGluLysLeu 43
Db 64 AATATAGAGATTACAGAGAGGAAATGAAACCGGATATCCAAAGTCCGCTGGATGCAAGCTC 123
Qy 44 GlnGluGluGlyGlySerAspGluGluGluThrGlySerProSerGluAspGlyMet 63

```

```

Db      124 GAAGAGCCCGGATCTGAGGCTGCCAGGAGGAGAAAG--GACCAAGACGGCGAG 180
Qy      64 GlnSerAlaArgThrGlnAlaArgProArgGluProLeuGluAspGlyAspProGluAsp 83
Db      181 ACCATGAGAGAGATCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Qy      84 AspArgThrLeu-----AspAspAspGluLeuAlaGluTyrAspLeuAspLys 99
Db      241 AAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Qy      100 TyrAsp---GluGluGluAspProAspAlaGlu-----ThrLeuGluGluSerLeuLeu 116
Db      301 TACGACGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
Qy      117 GlyLeuThrValTyrGlySerAspAspGlnAspProTyrValThrLeu---LysAspThr 135
Db      361 TCGCTGACGATCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 420
Qy      136 GluGlnTyrGluArgGluAspPheLeuLeuLysProSerAspPheLeuLeuValCysGly 155
Db      421 GAGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy      156 ArgAlaGluThrAspGlnCysAsnLeuGluValHisValTyrAsnGlnGluAspSer 175
Db      481 AAGGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
Qy      176 PheTyrValHisAspAlaLeuLeuSerAlaTyrProLeuSerValGluTyrLeuAsn 195
Db      541 CTTTACGTGACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 600
Qy      196 PheAsp-----ProSerProAspAspSerThrGlyAsnTyrLeuAlaValGlyAsn 212
Db      601 TTCCCTGTGGCGCACACGAGATGACCGAGCTACCGGCAATTCGTGGCGGTGAGAAC 660
Qy      213 MetThrProValIleGluValTyrAspLeuAspPheLeuValAspSerLeuGluProValPhe 232
Db      661 ATGAGAGCCGACATTTGAGTCTGGAGCTGGACATTTGACATGACATGACATGACATGACAT 720
Qy      233 ThrLeuGly-----SerLysLeuSerLysLysLysLysLysLysLysLysLysLysLys 245
Db      721 ATCTGAGGTGAGGCGGTGCGGAGCTGAGGAGAGACATGAAAGAGGCTTAAAGTCCAG 780
Qy      246 GlyLysLysSerSerSerAlaGluGlyHisThrAspAlaValLeuAspLeuSerTyrAsn 265
Db      781 AAGAGAGCCAGAGGAGATGACGATTCACGTCGACCGGTGCTGGCTGGCGCAAC 840
Qy      266 LysLeuIleArgAsnValLeuAlaSerAlaSerAlaAspAsnThrValIleLeuTyrAsp 285
Db      841 CGCCACACCGCAATGCTTGTGATCTGCATCCGCTGATCGTAAACCTCTGGGAC 900
Qy      286 MetSerLeuGlyLysProAlaAlaSerLeuAlaValHisThrAspLysValGlnThrLeu 305
Db      901 CTCAACACCGCCCAAGTGGCCAAATCTTACACCATATACGAGCAAGGTGCTGCTG 960
Qy      306 GlnPheHisProPheGlnAlaGlnThrLeuIleSerGlySerTyrAspLysSerValAla 325
Db      961 GACTGGACACCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Qy      326 LeuTyrAspCysArgSerProAspGluSerHisArgMetTyrArgPheSerGlyGlnIle 345
Db      1021 GCGGACACATGAGAGCTCCGACGCGAAGCGCGG---TGGGAGAGTGAATGCCGACGTC 1077
Qy      346 GluArgValThrTyrAsnHisPheSerProCysHisPheLeuAlaSerThrAspAspGly 365
Db      1078 GAGAGTGGCGGTGGATATTCACGACCCAACTTTCTATGTACACACGAGTCCGGT 1137
Qy      366 PheValTyrAsnLeuAspAlaArgSer-----AspLysProIle 378
Db      1138 ATGTCTTACCGCTACGATGTTTGAACATCCCTGCAACGCCAAGAGATGAAACCGGTC 1197
Qy      379 PheThrLeuAsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSerSerGlnIleLys 398
Db      1198 TGGACCTTGACGGCGCATGACACCTTGTGTATCTTTGACATCAACCTTGCAATTCCT 1257

```

```

Qy      399 GlyCysLeuValThrAlaSerAlaAspLysTyrValLysIleTyrAspIleLeuGlyAsp 418
Db      1258 GGCTTCTCTGTAACCGGATCAACGATTAAGCAAGTCAACTATGAACTCGGAATGCG 1317
Qy      419 ArgProSerLeuValHisSerArgAspMetLysMetGlyValLeuPheCysSerCys 438
Db      1318 CGGCTTACGATGATGCTCTCGGCTGAGATGACGTTGTGTAAGTGTGTTTCGACCACTTC 1377
Qy      439 CysProAsp-----LeuProPheIleTyrAlaPheGlyGlyGlnLysGluLeuArg 456
Db      1378 GCTCTGACACAGAGTGGCTTCGCGTGGCGGCTGACGACGAGGAGAACCGTCCAG 1437
Qy      457 ValTyrAspIleSerThrValSerSerValAsnGluAlaPheGlyArgArgGluArgLeu 476
Db      1438 ATCTGGACACCTCGACCAACGAGAGCGGTTCTGAGAGCTTTTGTGTCTGCAATGCCGCG 1497
Qy      477 ValLeuGlySerAlaArgAsnSerIleSerGlyProPheGlySerArgSerAsp 496
Db      1498 CTGGAAGCGGAGGTCAAGAGCGCACAAATCGAGTGCACCGACGATGATGAATCGAT 1557

```

RESULT 5

```

US-10-128-714-7208
; Sequence 7208, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wench
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroskinin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128, 714
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285, 697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287, 066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295, 890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303, 899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316, 362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7208
; LENGTH: 1629
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
; US-10-128-714-7208

```

Alignment Scores:

```

Pred. No.: 1,11e-101 Length: 1629
Score: 929.50 Matches: 206
Percent Similarity: 56.54% Conservative: 88
Best Local Similarity: 39.62% Mismatches: 197
Query Match: 35.21% Indels: 29
DB: 15 Gaps: 10

```

US-09-315-355c-10 (1-501) x US-10-128-714-7208 (1-1629)

```

Qy      4 SerArgGlnValThrCysValAlaTyrValArgCysGlyValAlaLysGluThrProAsp 23
Db      4 TCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 63
Qy      24 LysValGluLeuSerLysGluGluValLysArgGluIleAlaGluAlaLysGluLysLeu 43
Db      64 AATATATGAGATTGACGAGAGGAAATGAACCGGATATTCAGAGCTCGCTGGATGAGCTC 123

```



```

Db      64 AATATGAGATTGACGAGGAGAAATGACCGGATATTCAGCTTCGCTCGGATCGACGTC 123
Qy      44 GlnGluGluGlyGlyGlySerAspGluGluGluThrGlySerProSerGluAspGlyMet 63
Db      124 GAAAGAGCCGAGGTGATCTGAGAGCTGCCGAGGAGAAAG---GACACGAGAGCGGGAG 180
Qy      64 GlnSerAlaArgThrGlnAlaArgProArgGluProLeuGluAspGlyAspProGluAsp 83
Db      181 ACCATGAGGAGATCAGAGAGAGAAAGCCAGACCGGATGAGAGACGATTCGAGGAA 240
Qy      84 AsparGlnr----- 86
Db      241 AAGAGGG-AAAACAAGTTCAATGAGTAGCTCAAGCTTAAGTGTCCGATCTTCATA 299
Qy      87 -----LeuAspAspAspGluLeuAlaGluTyrAsp 96
Db      300 TAGACAAAGGCTAACACGTCATCTCGCTTCTTACTGATGAAAGATTGAAGAAATACGAC 359
Qy      97 LeuAspLysTyrAsp---GlnGluGlyAspProAspAlaGlu-----ThrLeuGlyGlu 113
Db      360 CTGATCATCTACGACAGATGATGAGGTGATGAGATGAGAGAGATCATCATGCTTCGGA 419
Qy      114 SerLeuLeuGlyLeuThrValTyrGlySerAspAspGlnAspProTyrValThrLeu--- 132
Db      420 AACGTCAAAGTCGCTAGCGTACACCAACCAAGAGAGATCCATACCTTGTATACCG 479
Qy      133 LysAspThrGluGlnTyrGluArgGluAspPheLeuIleLysProSerAspAspLeuIle 152
Db      480 GAAAGAGAGAGATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 539
Qy      153 ValCysGlyArgAlaGluGlnAspGlnCysAsnLeuGlnValHisValTyrAsnGlnGlu 172
Db      540 CTTCAGAGTAGTGTCGAGGATGAGGTGCCATCTTGAAGCTACGCTACGAGGACGAG 599
Qy      173 GluAspSerPheTyrValHisHisAspIleLeuLeuSerAlaTyrProLeuSerValGlu 192
Db      600 GAGCGCAACCTTTCAGTGCACACGACATTTAGTGCCTCCCTGCTGCTTGA 659
Qy      193 TrpLeuAsnPheAsp-----ProSerProAspAspSerThrGlyAsnTyrIleAla 209
Db      660 TGGCTGAGATTCCTGCTTGGCGCACACGAGATGCCGACCTACCGGAAATTTGATGCC 719
Qy      210 ValGlyAsnMetThrProValIleGluValTyrAspLeuAspIleValAspSerLeu 229
Db      720 GTAGGAACCATGAGCCCGACATTTAGGTCTGGACCTCGACATTTGATGATGATGATGAC 779
Qy      230 ProValPheThrLeuGly-----SerLysLeuSerLysLysLys 242
Db      780 CCAAAAGCCATCTGGGTCAAGGCGGTGCGAGCTCGAGGAGACATGAAAGGCTTAA 839
Qy      243 LysLysLysGlyLysLysSerSerSerAlaGluGlyHisThrAspAlaValLeuAspLeu 262
Db      840 AAGTCCAAAGAAAGAAAGCAAGGCGGATGACGAGTTCACGTCGATCTGCTGCTGCTG 899
Qy      263 SerTrpAsnLysLeuIleArgAsnValLeuAlaSerAlaSerAlaAspAsnThrValIle 282
Db      900 GCTGAAACCCGCAACACCGCATCTGCTGATTCGATCCGCGATCGATACCTTAA 959
Qy      283 LeuTrpAspMetSerLeuGlyLysProAlaAlaSerLeuAlaValHisThrAspLysVal 302
Db      960 CTCTGGACCTCAACACCGCCCAAGTGCCTTACACCCATCATACGAGCAAGGCTG 1019
Qy      303 GlnThrLeuGlnPheHisProPheGluAlaGlnThrLeuIleSerGlySerTyrAspLys 322
Db      1020 TGCTCGCTGAGCTGGACCTTAAAGAGCTACCGTTCCTCAGCGAGTTCATCATGATGT 1079
Qy      323 SerValAlaLeuTyrAspCysArgSerProAspGlnSerHisArgMetTrpArgPheSer 342
Db      1080 ACCGCTGGCGGCGGAGACATGAGCTCCGACCGGAAAGCCGG---TGGGAGATGAT 1136
Qy      343 GlyGlnIleGluArgValThrTrpAsnHisPheSerProCysHisPheLeuAlaSerThr 362
Db      1137 GCCGACGTCGAGAAATGTGGGTGATATTTCAGACCACTTCTTATGTCACACACA 1196

```

```

Qy      363 AspAspGlyPheValTyrAsnLeuAspAlaArgSer-----Asp 375
Db      1197 GATGCCGATGATGCTTACCCCTACGATGTTCGAAACATCCCTCCAAAGCCAAAGAAATCG 1256
Qy      376 LysProIlePheThrLeuAsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSerSer 395
Db      1257 AAACCGGTGAGACCTCGACGCGCATGACACTCTGTGTATTCCTTTGACATCAACCTT 1316
Qy      396 GlnIleLysGlyCysLeuValThrAlaSerAlaAspLysTyrValLysIleTrpAspIle 415
Db      1317 GCCATTCCTGCTTCTTCTTCGTAACCGATCAACGATTAAGCAATCAAGTATGAACGTC 1376
Qy      416 LeuGlyAspArgProSerLeuValHisSerArgAspMetLysMetGlyValLeuPheCys 435
Db      1377 GAGATGCGCGGCTGACATGATGTCGTCCTCCGTAAGATGAGACCTGGTAAAGTGTTCG 1436
Qy      436 SerSerCysCysProAsp-----LeuProPheIleTyrAlaPheGlyGlyGlnGlu 453
Db      1437 ACCACCTTCGCTCTGCAACGAGGTGGCTTCGCTGGCTGGAGCTGGACCAAGGGA 1496
Qy      454 GlyLeuArgValTyrAspIleSerThrValSerSerValAsnGluAlaPheGlyArg 473
Db      1497 ACCGTCGATCTGGGACACCTCGACCAACGAGCCGTTGTAGAGCTTTGTCTCCG 1556
Qy      474 GluArgLeuValLeuGlySerAlaArgAsnSerSerIleSerGlyProPheGlySerArg 493
Db      1557 ATGCCCGCCCTGGAAGCGGAGGTCAAGAGAGGACGACATCGAGTGCAGACGATGAT 1616
Qy      494 SerSerAsp 496
Db      1617 GAATCGGAT 1625

```

RESULT 7

```

US-10-128-714-208
; Sequence 208, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Mengli
; APPLICANT: Tienkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OR INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCES: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128, 714
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 208
; LENGTH: 3617
; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-208

Alignment Scores:
Pred. No.: 1,36e-98 Length: 3617
Score: 908.50 Matches: 207
Percent Similarity: 54.33% Conservative: 88
Best Local Similarity: 38.12% Mismatches: 196
Query Match: 34.41% Indels: 53

```


DB: 15 Gaps: 10
US-09-315-355C-10 (1-501) x US-10-128-714-208 (1-3617)
QY 4 SerArgInValThrCysValAlaTrpValArgCysGlyValAlaIleValGluThrProAsp 23
Db 1004 TCTTCTATGATCAGTACGACCGCTGGTGGCGGGGAGTGGCTGCGCAATTCCTTACC 1063
QY 24 LysValGluSerLysGluGluValLysArgLeuIleAlaGluAlaLysGluLysLeu 43
Db 1064 AAATATGATGATGAGAGAGAGAAATGAACCGATATCCAGTCCGCTCGATGACATC 1123
QY 44 GlnGluGlnGlyGlyGlySerAspGluGluGluThrGlySerProSerGluAspGlyMet 63
Db 1124 GAAGAGCCCGAGGATCTGAGGCTCCAGGAGGAAG---GACCAGAGCGGCGAG 1180
QY 64 GlnSerAlaArgThrGlnAlaArgProArgGluProLeuGluAspGlyAspProGluAsp 83
Db 1181 ACCATGAGAGGATCAGAGAGAGAGAGCCAGACCGGATGAGAGAGATTCGAGAGAA 1240
QY 84 AspArgThr----- 86
Db 1241 AAGAGGG-AAAAGACAGTTCAATGAGTACGCTTAAGCTTACGTCGATCTTATA 1299
QY 87 -----LeuAspAspAspGluLeuAlaGluThrAsp 96
Db 1300 TAGACAAGGCTAACCTGATCTCGCTTGTAGTGAATTTGAAGAATACGAC 1359
QY 97 LeuAspLysThrAsp---GluGluGluAspProAspAlaGlu-----ThrLeuGlyGlu 113
Db 1360 CTTATCATCACTACGACGATGAGATGATGATGAGAGAGATCATCATCATCTTCCGA 1419
QY 114 SerLeuGlnGlyLeuThrValThrGlySerAspGlnAspProGlyValThrLeu--- 132
Db 1420 AACGCTCAAGTCTGATGCTACCAACCAACCAAGAGATTCATACCTTGTATACCG 1479
QY 133 LysAspThrGlnGlnGlnGluArgGluAspPheLeuIleLysProSerAspAsnLeuIle 152
Db 1480 GAAGAGAGAGAGATGAAAGAGAGAGAGAGATTCCTCCACCGACCACTTGGCT 1539
QY 153 ValCysGlyArgAlaGluGlnAspGlnCysAsnLeuGluValIleValThrAsnGln 172
Db 1540 CTTCCAGGTAAAGTCCAGAGATGAGTGGCCCATCTTGAAGCTACGCTTACGAGACAG 1599
QY 173 GlnAspSerPheThrValHisHisAspIleLeuSerAlaThrProLeuSerValGlu 192
Db 1600 GAGGCGAACCTTTACGTCACCAACGATATGCTGCCCGCCATCCCTGTGCTTGA 1659
QY 193 TrpLeuAsnPheAsp-----ProSerProAspAspSerThrGlyAsnThrIleAla 209
Db 1660 TGGCTGGATTTCCCTGTTGGCGCACACGATACCGGATACCGGCAATTCGTGGCC 1719
QY 210 ValGlyAsnMetThrProValIleGluValTrpAspLeuAspIleValAspSerLeuGlu 229
Db 1720 GTAGAACCAATGAGCCCGACATTCGAGGCTGAGACCTGAGCATTTGCTGATCATGAT 1779
QY 230 ProValPheThrLeuGly-----SerLysLeuSerLysLys 242
Db 1780 CCAAAAGCCATCTGGGTCCAGGGCGGTGGAGCTCCAGGAGACATGAAAGAGCTTAA 1839
QY 243 LysLysLysGlyLysLysSerSerSerAlaGluGlnHisIleThrAspAlaValLeuAspLeu 262
Db 1840 AAGTCCAAAGAGAGAGAGAGAGAGAGAGAGATTCACGTCGATCCGCTGCTGCTGG 1899
QY 263 SerTrpAsnLysLeuIleArgAsnValLeuAlaSerAlaSerAlaAspAsnThrValIle 282
Db 1900 GCTCAAAACCCGCAACCCGCAATCTGCTCATCTGATCCGCTGATCCGATGAAA 1959
QY 283 LeuTrpAspMetSerLeuGlyLysProAlaIleSerLeuAlaValHisIleThrAspVal 302
Db 1960 CTTGGGACCTCAACACCGCAAGTGGCCCAATTTACCACTTCATACGAGAGAGGTG 2019
QY 303 GlnThrLeuGlnPheHisProPheGluAlaGlnThrLeuIleSerGlySerThrAspLys 322

Db 2020 TGCTCGTGACATCGGACACCTTAAGAGATACCGTTCTCTCACCGGATTTACGATCGT 2079
QY 323 SerValAlaLeuThrCysArgSerProAspGluSerHisArgMetTrpAspPheSer 342
Db 2080 ACCGTGTGGCGGACAGCATGAGAGCTCCGAGCCGAAAGCGG---TGGGAGTGAT 2136
QY 343 GlyGlnIleGluArgValThrTrpAsnHisPheSerProCysHisPheLeuAlaSerThr 362
Db 2137 GCGGACGTGAGAAATGGCGGTGGATATTCACGACCCAAACTTCTTATGTCACACACA 2196
QY 363 AspAspGlyPheValIleThrLeuAspAlaArgSer-----Asp 375
Db 2197 GATGCCGTGTGTCTTACCCGCTACAGATGTTGAAACATCCCTGCAACGCCAAAGATCG 2256
QY 376 LysProIlePheThrLeuAsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSerSer 395
Db 2257 AAACCGGTCTGACCTTCCGAGGCGCATGACACCTCTGTGTATCTTTGATCATCAACCT 2316
QY 396 GlnIleLysGlyCysLeuValThrAlaSerAlaAspLysThrValIleThrAspIle 415
Db 2317 GCCATTCTGCTTCTCTCGTAAACCGGATCAACGATTAAGCAATCAAGTATGAAAGTTC 2376
QY 416 LeuGlyAspArgProSerLeuValHisSerArgAspMetLysMetGlyValLeuPheCys 435
Db 2377 GAGATGCGCGGCTTACGATGCTGCTCGCTGATGATGATGATGATGATGATGATGATG 2436
QY 436 SerSerCysSerProAsp-----LeuProPheIleThrAlaPheGlyGlnLysGlu 453
Db 2437 ACACCTCTGCTCTTGAACAGAGAGTGGCTTCCGTTGGCGGTAGCTGACAGCAAGGA 2496
QY 454 GlyLeuArgValTrpAspIleSerThrValSerSerValAsnGluAlaPheGlyArgArg 473
Db 2497 ACCGTCAAGTCTGGAGACCTGACCAACGAGAGCGGTTGTAGAGTTTGTGTCTCGC 2556
QY 474 GlnArgLeuValLeuGlySerAlaArgAsnSerSerIleSerGlyProPheGlySerArg 493
Db 2557 ATGCCCGCCCTGAGAGAGCGAGTCAAGAGAGCGACATCGAGTGCAGCCGATGAT 2616
QY 494 SerSerAsp 496
Db 2617 GAATCGAT 2625

RESULT 8
US-10-128-714-5208
; Sequence 5208, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengli
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128, 714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5208
; LENGTH: 3697


```

; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
; US-10-128-714-5208

Alignment Scores:
Pred. No.: 1.41e-98 Length: 3697
Score: 908.50 Matches: 207
Percent Similarity: 54.33% Conservative: 88
Best Local Similarity: 38.12% Mismatches: 196
Query Match: 34.41% Indels: 53
DB: 15 Gaps: 10

US-09-315-355c-10 (1-501) x US-10-128-714-5208 (1-3697)

QY 4 SerArgInValThrCysValAlaTrpValArgCysGluValAlaLysGluThrProAsp 23
Db 1004 TCTTCTATGATCACTACGACCGCTTGGGTGCGGGGAGACTCGTCCCAATCCCTACC 1063
QY 24 LysValGluLeuSerLysGluValLysArgLeuLeaIaGluAlaLysGluLysLeu 43
Db 1064 AAATATGATTTGACGAGGAGAAATGAACCGGATATCCAAAGCTCGCTCGATGACAGCTC 1123
QY 44 GlnGluGluGlyGlySerAspGluGluGluThrGlySerProSerGluAspGlyMet 63
Db 1124 GAAGAGGCCCGAGGTGATCTGAGGCTGCCAGGAAAGAAAG--GACGAGGACGGCGAG 1180
QY 64 GlnSerAlaArgThrGlnAlaArgProArgGluProLeuGluAspGlyAspProGluAsp 83
Db 1181 ACCATGAGAGAGATCGAAGAGAGAAAGCCCAAGCCGATGAGAGACGATTCGAGAGAA 1240
QY 84 AspArgThr----- 86
Db 1241 AAGAAAGG-AAAAGACAGTTTCAATGATAGTGTAAAGCTAGTGTCCGATCTTCATA 1299
QY 87 -----LeuAspAspAspGluLeuAlaGluThrLeuGlyGlu 113
Db 1300 TAGACAGGCTAACACTGATCTCGCTTGTGATGATGAAGATTGAAAGAAATACGAC 1359
QY 97 LeuAspLysThrAsp---GluGluGlyAspProAspAlaGlu-----ThrLeuGlyGlu 113
Db 1360 CTGATCACTACGACGATGATGAGTGTAGAGATGAGAGAAAGATACCATGTTGGGA 1419
QY 114 SerLeuGluGlyLeuThrValThrGlySerAsnAspAspProThrValThrLeu--- 132
Db 1420 AACGTCAAGTCGCTACGCTACCAACCAACGAGAGAAATCATCTTGTGATACCG 1479
QY 133 LysAspThrGluGluThrValThrGluArgGluAspPheLeuLeuLysProSerAspAsnLeu 152
Db 1480 GAAGAAAGAAAGATGAAAGAGAGAGAGATGTCAGATCTTCCACCGCAACTTGTCTT 1539
QY 153 ValCysGluArgAlaGluGlnAspGlnCysAsnLeuGluValHisValThrAsnGlnGlu 172
Db 1540 CTTCAGATTAAGTGCAGATGAGTGGCCCATCTTAAGCTTACGTCCTACGAGACAG 1599
QY 173 GlnAspSerPheThrValHisHisAspIleLeuLeuSerAlaThrProLeuSerValGlu 192
Db 1600 GAGCGCAACCTTTCACGTCACACGATATGCTGCCGCCACCTCTGTGCTTGAA 1659
QY 193 TrpLeuAsnPheAsp-----ProSerProAspAspSerThrGlyAsnThrIleAla 209
Db 1660 TGGCTGATTTCCCTGTTGGCGCACACACGATGACCGGCAATTTGCTGGCC 1719
QY 210 ValGlnAsnMetThrProValIleGluValTrpAspLeuAspIleValAspSerLeuGlu 229
Db 1720 GTAGAAACCATGAGCCCGACATTGAGGTCTGGACCTGACATTTGTCAGCTGCATATAC 1779
QY 230 ProValPheThrLeuGly-----SerLysLeuSerLysLys 242
Db 1780 CCAAAACCCATCTCTGGGTACAGGGCGGTGCGGAGCTCGAGGAGACATGAAGAAAGCTAAA 1839
QY 243 LysLysLysGlyLysLysSerSerSerAlaGluGlyHisThrAspAlaValLeuAspLeu 262
Db 1840 AAGTCCAAAGAAAGACCAAGGCGAATGACGATTCCACGTCGCTCGCTCGCTTG 1899

```

```

QY 263 SerTrpAsnLysLeuIleArgAsnValLeuAlaSerAlaSerAlaAspAsnThrValIle 282
Db 1900 GCTGCMAACCGCCACACCGCAATCTGCTGCATCGATCCGCTGATCCGTAATAA 1959
QY 283 LeuTrpAspMetSerLeuGlyLysProAlaAlaSerLeuAlaValHisThrAspLysVal 302
Db 1960 CTCTGGACCTCAACACCGCCCAAGTGGCCCAATCTTACCAACCATCATACGAAAGGTG 2019
QY 303 GlnThrLeuGlnPheHisProPheGlnAlaGlnThrLeuIleSerGlySerThrAspLys 322
Db 2020 TGTCTGCTGACTGCGACCCCTTAAGAGACTTACCGTTCTCTCCACCGTATGATTCCT 2079
QY 323 SerValAlaLeuThrAspCysArgSerProAspGluSerHisArgMetTrpArgPheSer 342
Db 2080 ACCGTGTGCGGCGACATGAGAGAGCTCCGACCGGAAAGCCCG--TGGGAGTGGAT 2136
QY 343 GlnGlnIleGluArgValThrTrpAsnHisPheSerProCysHisPheLeuAlaSerThr 362
Db 2137 GCCGAGTCGAGAAATGTGGTGGATATTCAAGACCCAACTTCTTATGTACACACA 2196
QY 363 AspAspGlyPheValThrAsnLeuAspAlaArgSer-----Asp 375
Db 2197 GATGCCGATGATGATCTACCGCTACGATGTCGAACATCTCTGCAACGCCAAAGATCG 2256
QY 376 LysProIlePheThrLeuAsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSerSer 395
Db 2257 AAACGGTGTGACCCCTGACGCGCATGACACTCTGTCTATCTTTCATCACTCAACCT 2316
QY 396 GlnIleLysGlyCysLeuValThrAlaSerAlaAspLysThrValLysIleThrAspIle 415
Db 2317 GCCATCTCTGCTCTCTCTTAACCGGATCAAGGATTAACCAAGTCAAGCTATGAAAGCTC 2376
QY 416 LeuGlyAspArgProSerLeuValHisSerArgAspMetLysMetGlyValLeuPheCys 435
Db 2377 GAGATGCGCGGCTACGATGATGCTCTGCGTGAAGATGAGAGTGTGTAAGTGTTCG 2436
QY 436 SerSerCysAspProAsp-----LeuProPheIleThrAlaPheGlyGlyGlnGlu 453
Db 2437 ACCACCTTGCTCTTACACACAGAGTGGCTTCGCTTGGCGGTAGCTGGACAAAGGA 2496
QY 454 GlnLeuArgValTrpAspIleSerThrValSerSerValAsnGluAlaPheGlyArgArg 473
Db 2497 ACCGTCAAGATCTGGACACCTCGACCAACGAGCGGTCGTAGAGCTTTTGTCTCGC 2556
QY 474 GlnArgLeuValLeuGlySerAlaArgAsnSerSerIleSerGlyProPheGlySerArg 493
Db 2557 ATGCCCGCCCTGGAAGCGAGGTCAAGAGCGACATGCGAGTGCAGACCGACATGAT 2616
QY 494 SerSerAsp 496
Db 2617 GAATCGGAT 2625

RESULT 9
US-10-128-714-1208
; Sequence 1208, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wengli
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshekin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128, 714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27

```

PRIOR APPLICATION NUMBER: US 60/295,890
 PRIOR FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: US 60/303,899
 PRIOR FILING DATE: 2001-07-09
 PRIOR APPLICATION NUMBER: US 60/316,362
 PRIOR FILING DATE: 2001-08-31
 NUMBER OF SEQ ID NOS: 8603
 SOFTWARE: Patent version 3.1
 SEQ ID NO 1208
 LENGTH: 1617
 TYPE: DNA
 ORGANISM: Aspergillus fumigatus
 US-10-128-714-1208

Alignment Scores:

Pred. No.:	5 03e-99	Length:	1617
Score:	907.50	Matches:	205
Percent Similarity:	54.97%	Conservative:	88
Best Local Similarity:	38.46%	Mismatches:	188
Query Match:	34.38%	Indels:	53
		Gaps:	10

US-09-315-355c-10 (1-501) x US-10-128-714-1208 (1-1617)

QY 4 SerArgGlnValThrCysValAlaIleArgCysGlyValAlaIleGluThrProAsp 23
 Db 4 TCTTCTATGATCATTACGACCGCTTGCGTGGCGGGAGTCGCTGCCCAATTCCTACC 63
 QY 24 LysValGluLeuSerLysGluGluValLysArgLeuIleAlaGluAlaLysGluLysLeu 43
 Db 64 AAATATGATGATTGACGAGAGAAATGAAACCGATATCCAGCTCGCTCGATCCAGCTC 123
 QY 44 GlnGluGluGlyGlySerAspGluGluGluThrGlySerProSerGluAspGlyMet 63
 Db 124 GAAGGCGCCAGGGGATCTGAGGCTGCCAGGAGGAAG--GACCAGAGCGGAG 180
 QY 64 GlnSerAlaArgThrGlnAlaArgProArgGluProLeuGluAspGlyAspProGluAsp 83
 Db 181 ACCATGAGAGAGATCAGAGAGAAAGAACCCAGACCGGATGAGAGCATTCGAGAGAA 240
 QY 84 AspArgThr----- 86
 Db 241 AAGAAGGG-AAAGACAAGTTCAATGAGTAGCTTAAGCTTAGTTCGCATCTTATA 299
 QY 87 -----LeuAspAspAspGluLeuAlaGluThrAsp 96
 Db 300 TAGACAAGGCTTAACACGTCATCTCGCTTGTAGTGAAGATTGAAAGAAATACGAC 359
 QY 97 LeuAspLysIleAsp---GluGluGlyAspProAspAlaGlu-----ThrLeuGlyGlu 113
 Db 360 CTTGATCTACAGACAGATGAGATGAGTGCATGAGATGAGAGAAAGATCACCATCTTCCGA 419
 QY 114 SerLeuGluGlyLeuThrValIleGlySerAspGluAspProIleValThrLeu--- 132
 Db 420 AACGTCAGATGCTAGCGTACCAACCAACGAGAGAAATCATATCTTGATATACG 479
 QY 133 LysAspThrGluGluGluGluGluAspLeuIleLysProSerAspAspLeuIle 152
 Db 480 GAAGAAGAGAGATGAGAGAGAGAGAGAGTTCAGATCTTCCACCGACCACTTCTCT 539
 QY 153 ValCysGlyArgAlaGluGluAspGlnCysAsnLeuGluValAlaIleValIleAsnGlu 172
 Db 540 CTTGCAAGTAAAGTCGAGATGAGATGAGTGCATCTTGAAGCTTACGTTACGAGACAG 599
 QY 173 GluAspSerPheIleValIleHisAspIleLeuLeuSerAlaIleProLeuSerValGlu 192
 Db 600 GAGGGAACCTTACGTCACCAAGCATTAAGTCCGCCGCCATCCCTGCTGCTGCTGAA 659
 QY 193 TrpLeuAsnIleAsp-----ProSerProAspAspSerThrGlyAsnIleAla 209
 Db 660 TGGCTGGATTTCCCTGTTGGCGACACACGATGATGACCGGGAATTTGGTGGCC 719
 QY 210 ValGlyAsnMetThrProValIleGluValIleTrpAspLeuAspIleValAlaAspSerLeuGlu 229

Db 720 GTAGGAACCATGAGCGCCGACATGAGTGTGGAGACTGGACATTCGATCGATCATGTAC 779
 QY 230 ProValPheThrLeuGly-----SerLysLeuSerLysLys 242
 Db 780 CCAACCGCATCTCTGGTTCAGGCGCGTGGAGCTCGAGCTGAGAGACATGAAGAGCTTAA 839
 QY 243 LysLysLysGlyLysLysSerSerSerAlaGluGlyHisThrAspAlaValLeuAspLeu 262
 Db 840 AAGTCCAGAGAGAAAGCAAGGAGATGACGATTCACAGTTCACGTCGATCCGCTCGCTTG 899
 QY 263 SerTrpAsnLysLeuIleArgAsnValLeuAlaSerAlaSerAlaAspAsnThrValIle 282
 Db 900 GCTCAAAACCGCCACACCGCAATCTGCTGATGCAATCCCTGATCCCTACCGTAAAA 959
 QY 283 LeuTrpAspSerSerLeuGlyLysProAlaIleSerLeuAlaValHisThrAspLysVal 302
 Db 960 CTCTGGGACCTCAACACCGCCAAAGTGGCCAAATTTACACCCATCATACGACCAAGGTG 1019
 QY 303 GlnThrLeuGlnPheHisProPheGluAlaGlnThrLeuIleSerGlySerIleAspLys 322
 Db 1020 TGCTCGTGAGCTGCGACACCTTAAGAAAGTACCGCTTCTCTCAACCGGATTCGATCGT 1079
 QY 323 SerValAlaLeuThrAspCysArgSerProAspGluSerHisArgMetTrpArgPheSer 342
 Db 1080 ACCGTGTGCGGCGACAGATGAGAGCTCCGACGCAAAAGCGCG--TGCGGAGTGGAT 1136
 QY 343 GlyGlnIleGluArgValThrTrpAsnHisPheSerProCysHisIlePheLeuAlaSerThr 362
 Db 1137 GCGGACGTCGAGATGCGCGTGGATTCACGACCCAACTTCTTATGTCACCA 1196
 QY 363 AspAspGlyPheValIleAsnLeuAspAlaArgSer-----Asp 375
 Db 1197 GATCGCGATGATGATCTTACCCCTACGATGTTGGAACATCCCTGCAAGCCAAAGATCG 1256
 QY 376 LysProIlePheThrLeuAsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSerSer 395
 Db 1257 AAACCGGTGACACCTGCGAGCGCATGACACCTGTGTCATCTTGCATCAACACCT 1316
 QY 396 GlnIleLysGlyLysLeuValThrAlaSerAlaAspLysIleThrPheAla 415
 Db 1317 GCCATTCCTGGCTTCTCTGTAACCGGATCAACGGAATGCAAGTCAAGTATGAAAGCT 1376
 QY 416 LeuGlyAspArgProSerLeuValHisSerArgAspMetLysMetGlyValLeuPheCys 435
 Db 1377 GAGAAAGCGCGCTTACAGATGCTGCTCCGTAAGATGAGCTTGTAAAGCTTTTCG 1436
 QY 436 SerSerCysAspProAsp-----LeuProPheIleThrAlaPheGlyGlnLysGlu 453
 Db 1437 ACACACTTGCCTCTGCAACAGAGTGGCTTCGCTGGCGGTAGCTGACAGCAAGGA 1496
 QY 454 GlyLeuArgValTrpAspIleSerThrValSerSerValAsnGluAlaPheGlyArg 473
 Db 1497 ACCGTCCAGTTCGGGACACCTTGACCAAGAGCGGTTCGTAGACCTTTGTGCTCGC 1556
 QY 474 GluArgLeuValLeuGlySerAlaArgAsnSerIle 486
 Db 1557 ATGCCCGCCCTGGAAGGCGAGTCAAGAGCGCACATC 1595

RESULT 10
 US-09-949-029-59
 Sequence 59. Application US/09949029
 Publication No. US20030134278A1
 GENERAL INFORMATION:
 APPLICANT: Karpen, G.H.
 APPLICANT: Dobie, K.W.
 APPLICANT: Kennedy, C.D.
 APPLICANT: Velasco, V.M.
 APPLICANT: McGrath, T.L.
 APPLICANT: Meko, J.
 APPLICANT: Patterson, R.W.
 TITLE OF INVENTION: Identification of chromosome inheritance modifiers in Drosophila

DB: 13 Gaps: 22
 US-09-315-355c-10 (1-501) x US-10-032-585-6502 (1-1839)
 Qy 7 ValThrcysValAlaTTPValArgCysGlyValAlaLysGluThrProAspLysValGlu 26
 Db 4 ATTTCTTCAAGTGGTGGTTCGCAAGGGGTTTCTGCTCGCAATTCCTCCAGAAATATGAA 63
 Qy 27 LeuSerLysGluValLysArgLeuLeuA-----GluAla 39
 Db 64 TTAGATGATGAAGAAATGGAAGAAATCATCCATGCCCATTTAGAACTTAATGATGCC 123
 Qy 40 LysGluLysLeuGluGluGlyGlyGlySerAspGluGluThrGlySerProSer 59
 Db 124 AAAAGAACATTAAGCAGAGCAGAGGT-----GAGAGAGAAACA----- 162
 Qy 60 GluAspGlyMetGlnSerAlaArgThrGlnAlaArgProArgGluProLeuGluAspGly 79
 Db 163 -----GAGACCAAT 171
 Qy 80 Asp-----ProGluAspAspArgThrLeuAsp-----AspAspGlu 91
 Db 172 GATTGGGGGATGCCCAAAACATCTAAATTAAGTGAACAATTTGAATGATGATGAT 231
 Qy 92 LeuAlaGluTyraAspLysAspLysTyraSp--GluGluGlyAspProAspAlaGluThr 110
 Db 232 TTAAAGAAATATGATTTAGAAATTAATGATGATGATGATGATGATGATGATGAT 291
 Qy 111 LeuGluGlySerLeuLeuGlyLeuThrValTyrlGlySerAsn----- 124
 Db 292 TTAGAAATATCTAAATCTCCATGTCCAGTTTATCCATTAAGTGAATTAATTA 351
 Qy 125 -----AspGlnAspProTyraValThrLeuLysAsp-----ThrGluGln 137
 Db 352 CAATGATGAAGTGAAGAGAGTGAATTAATTAATTAATTAATTAATTAATTAATTA 411
 Qy 138 TyrlGluArgGluAspPheLeuLeuLysProSerAspAsnLeuLeuValCysGlyArgAla 157
 Db 412 GAGAGAAAGAAAGAAATCAAAATTTATCCAGTGAATTAATTAATTAATTAATTA 471
 Qy 158 GluGluGlnGlyCysAsnLeuGluValHisValTyraAsn----- 170
 Db 472 GAGATGATATATCTTGGTGGATATTAATTAATTAATTAATTAATTAATTAATTA 531
 Qy 171 -----GlnGluGluAsp----- 174
 Db 532 GGTCTGAGAGAGAGAGAGAGATTAATTAATTAATTAATTAATTAATTAATTA 591
 Qy 175 -----SerPheTyraValHisAspLysLeuLeuSerAlaTyrlProLeuSerValGlu 192
 Db 592 GAATCAAAATTTGTATGTACCATGATATCAATGTTTACCTGCCATTTATGTGTGAA 651
 Qy 193 TrpLeuAsnPheAspProSerProAspAspSerThr--GlyAsnTyrlLeuAlaValGly 211
 Db 652 TGGATTAATTAATTAATCAAGGTCAAGAACATCAATATTAATTAATTTGCTGCTATGCT 711
 Qy 212 AsnMetThrProValLysGluValTyraAspLysAspLysAspSerLeuGluProVal 231
 Db 712 ACTTTGACCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 771
 Qy 232 PheThrLeuGly-----SerLysLeuSerLys 240
 Db 772 GTATATTTGGGTGAACCAATATAAATTCATTCATAGCTAAAGAAATTAATTAATTA 831
 Qy 241 LysLysLysLysLysGlyLysLysSerSerSerSerSerSerSerSerSerSerSer 260
 Db 832 AAAAG 885
 Qy 261 AspLeuSerTrpAsnLysLeuLeuLysAsnValLeuAlaSerAlaSerAlaAspAsnThr 280
 Db 886 TCCTTTGACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 945
 Qy 281 ValLeuLeuTrpAspMetSerLeuGlyLysProAlaAlaSerLeu--AlaValHisThr 299

Db 946 GTGAAATTAATGAGATTTGAACAGTCTACTGCTGTTGTTGCTGTTGTAATAATTCATCAT 1005
 Qy 300 AspLys-----ValGlnThrLeuGlnPheHisLeuProPheGlyValAlaGlnThrLeuLysSerGly 318
 Db 1006 AATTAAGTCTTCAATCTTCTCAATGAGCATTTCAAGAGAACATCTATTATTATGACAGCT 1065
 Qy 319 SerTyraAspLysSerValAlaLeuTyraSpCysArg----- 330
 Db 1066 GGATATGATTTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1125
 Qy 331 SerProAspGluSerHisArgMetTrpArgPheSerGly--GlnLysGluArgValThr 349
 Db 1126 TCATCAGATTTCTTAACCAATTAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1185
 Qy 350 TrpAsnHisPheSerProCysHisPheLeuAlaSerThrAspAspGlyPheValTyraAsn 369
 Db 1186 TGGATCTTCTTAACCAAGATTAATTTATGCGGAGTACATGATATGATATGATATGATACGT 1245
 Qy 370 LeuAspAlaArgSerAsp--LysProLysPheThrLeuAsnAlaHisAsnAspGluLe 388
 Db 1246 TTGATATTCAGACAGAGATTTCTAAGCCATTAATGATGATGATGATGATGATGATGATG 1305
 Qy 389 SerGlyLeuAspLysSerSerGlnLysGlyCysLeuValThr--AlaSerAlaAsp 407
 Db 1306 TCTTCATTTGACCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1365
 Qy 408 LysTyraValLysLysLeuTrpAspLysLeuGlyAspArg----- 419
 Db 1366 AAGATGATCAAACTTTGGAATATGCCCTTCATCTGATGATGAATAACACCAACCAAAAA 1425
 Qy 420 -----ProSerLeuValHisSerArgAspMetLysMetGlyValLeuPheCysSerSer 437
 Db 1426 CAAGTCTCTTCCATGCTTTGTCGAGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1485
 Qy 438 CysCysProAspLeuProPheLeu-----TyraLysPheGlyGlyGlnLysGluGlyLeu 455
 Db 1486 TATGCTCTTATTAATGAAGTGTGCTGATATGATGATGATGATGATGATGATGATGATG 1545
 Qy 456 ArgValTrpAspLysSerThrValSerSerValAsnGluAlaPheGlyArgArgGluArg 475
 Db 1546 AAGATGCGGATGATTCATTCATTAATTAATTAATTAATTAATTAATTAATTAATTA 1605
 Qy 476 LeuValLeuGlySerAlaArgAsn-----SerSerLysSer 487
 Db 1606 GATTAACAAATATATGCTAGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1665
 Qy 488 GlyProPheGlySerArgSerSer 495
 Db 1666 AGAAATATTAACAGCAATTAATTAAT 1689
 RESULT 12
 US-10-320-797-2234
 Sequence 2234, Application US/10320797
 Publication No. US20040014955A1
 GENERAL INFORMATION:
 APPLICANT: Zamedio, Carlos
 APPLICANT: Eroshkin, Alexey M.
 TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
 FILE REFERENCE: 10182-021-999
 CURRENT APPLICATION NUMBER: US/10/320, 797
 CURRENT FILING DATE: 2002-12-16
 PRIOR APPLICATION NUMBER: 60/341,261
 PRIOR FILING DATE: 2001-12-17
 NUMBER OF SEQ ID NOS: 3361
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 2234
 LENGTH: 1638
 TYPE: DNA
 ORGANISM: Cryptococcus neoformans
 US-10-320-797-2234


```

; TYPE: DNA
; ORGANISM: Cryptococcus neoformans
; US-10-320-797-234

Alignment Scores:
  Pred. No.:      2.05e-74      Length:      3292
  Score:          708.00        Matches:      176
  Percent Similarity: 47.87%    Conservative: 116
  Best Local Similarity: 28.85%  Mismatches:   171
  Query Match:     26.82%      Indels:       149
  DB:              12          Gaps:         15

US-09-315-355c-10 (1-501) x US-10-320-797-234 (1-3292)

Qy      7 ValThrCysValAlaIATrPValArgCysGlyValAlaIatysgluThrProAspLysValGlu 26
Db      1016 ATTCTTCCTCCGTATGGGTTCCAGAGCCGCTCGCGGGAACCAAAATATATACAG 1075
Qy      27 LeuSerLysgluValLysArgLeu-----
Db      1076 CTCGATGAAGACGAGATCGAAGCTGTAGCGCAAGCTCGCGGCTGTGTTCGAAACAG 1135
Qy      36 -----
Db      1136 CTCGAAGCTGAGATAGCGGCTGTGAGAGATGTGAAGAGATGAGGCGATGAGAGAA 1195
Qy      52 GluGluGluThrGlySerProSerGluAspGlyMetGlnSerAlaArgThrGlnAlaArg 71
Db      1196 GAGAGCTGGGAGGACGAGAGATGACGAAAGAGGTATATGAGGAGGACAAATGACGATGAC 1255
Qy      72 ProArgLupProLeuGluAspGlyAspProGluAspAspArgThrLeuAspAspGlu 91
Db      1256 GACGAGAAGATGATGAAGACAGAGAGCCGAG-----AAGCATTTTGAACCTTAATGAC 1309
Qy      92 LeuAlaGluTyrAspLeuAspLysTyrAspGluGluGlyAspProAspAlaGluThrLeu 111
Db      1310 CTATCACTCTTCAAGATGAGACGAATACGATGAAAG-----GAGTCCAAAGCGGTT 1360
Qy      112 GlyGlu-----
Db      1361 GGTAAGATTTTATCGTATGATATCAATTATGTTAAAGCTGACCGAAATGACGCGATGGTCT 1420
Qy      114 -----SerLeuLeuGlyLeuThrValTyrGlySerAsnAspGluAspProTyrValThr 131
Db      1421 TTGCGCAACATCAAGAGTGTGACATATATATCGGACAAAGAAATCATATATACACC 1480
Qy      132 LeuLysAspThr-----
Db      1481 CTCAAGGAGGT-TCGTGTCTTGCTGCTGATGATATCAACGAAATGGCCCATCGGCTAAT 1539
Qy      136 -----GluGlnTyrGluArgGluAspPheLeuLileLysProSerAsp 149
Db      1540 TCGTTTAAACGATGAAGAAAGAAACGAGACGAGGCTGTGTTCTCTCCCAACAGAT 1599
Qy      150 AsnLeuIleValLysGlyArgAlaGluGlnAspGlnCysAsnLeuGluValHisValTyr 169
Db      1600 TCTATGATTAATCTCTGCGCGAAGACCTCCGACCTTCATCCCTCGATTTCCATGTCTAC 1659
Qy      170 AsnGlnGluAspSerPheTyrValHisHisAspLileLeuLeuSerAlaTyrProLeu 189
Db      1660 GCCGATGCGAGAAACCTTATAGCGACCATGACCTTATGCTTCGCTCCCTCCCTG 1719
Qy      190 SerValGluTyrPheAsnPheAspProSerProAspAspSer-----
Db      1720 TGTGTGATGATGCTAGACTTCTCTCTGCTCTGATGCAACGCTGCTCCGGAAGGC 1779
Qy      204 -----ThrGlyAsnTyrIleAlaValAlaGlyAsnMetThrProValIleGluValTyrAsp 221
Db      1780 GCTAAGCCCGGTACTACTGCTGCTGCTGCTCTTTCGACCCCAAGATGAAATATGGAT 1839
Qy      222 LeuAspLileValAspSerLeuGluProValPheThrLeuGlySerLysLeuSer----- 239
Db      1840 GCCGACCTGTTGATGTCTTATCCCGGGCTATCTCGGCCCATCATCATTCCGCTTGA 1899
```

```

Qy      240 -----LysLysLysLysLysLysGlyLysLys 248
Db      1900 AAGCAGAGGCCAAACCCCTTGGTACCGGTAAAGAAAGCAAAATGATACAGCCT 1959
Qy      249 SerSerSerLileGluGlyHisThrAspAlaValLeuAspLeuSerThrAsnLysLeuIle 268
Db      1960 GCTGCCAAGCCGACATCAACATGTCAGCCCGCTCTTCTCTTCGAGACCCCAATCAC 2019
Qy      269 ArgAsnValLeuLileSerAlaSerAlaAspAsnThrValIleLeuTyrPheMetSerLeu 288
Db      2020 CGAAACCTGCTCTTCTCCGTTCTGCGGACGATCATCAAACTTGGATTGACCTCGT 2079
Qy      289 GlyLysPheAlaAlaSerLeu-----AlaValHis---ThrAspLysValGln 303
Db      2080 GAATCAACCCATGGGTGTATGCGCAGCTGGACAAAGSTCATGATGTAAGATTCAG 2139
Qy      304 ThrLeuGlnPheHisProPheGluAla-----GlnThrLeuLileSerGlySer 319
Db      2140 GCTGTGAGTGGAAACAGAGACACCGTCGCGGCTTTGGACAAAGTCTGCTGAGTGCAGGT 2199
Qy      320 TyrAspLysSerValAlaLeuTyrAspCysArgSerProAspGluSerHisArgMetTyr 339
Db      2200 TATGACGAGACGGTCAAGGTTTGGATGGCGAGCCGCTGACGAACTATCGGATG--- 2256
Qy      340 ArgPheSerGlyGlnIleGluArgValThrTyrAsnHisPheSerProCysHisAspLeu 359
Db      2257 CAAGTCCTAGTACANTGATGATGTGTGATGGAACCAATGGAGCCTTATCTC-TTTCTA 2315
Qy      359 -----
Db      2316 CGTACGTTAAGCTATCCCGAGCTAGATATCAAGCTCAAGCTTAATGATGATGCTAG 2375
Qy      360 AlaSerThrAspAspGlyPheValTyrAsnLeuAspAlaArg----- 373
Db      2376 GTTCTTGGAGATGTGCTCATTTCTCTCTTACGACTCTGAGTCTCTCATCTCCAAA 2435
Qy      374 -----SerAspLysPro 377
Db      2436 TCGCATCTCTGCTACAGGCTCTCCCAAGTCCCTGCTCTCTTACTACCGCTCAACCT 2495
Qy      378 IlePheThrLeuAsnAlaHisAsnAspGluLileSerGlyLeuAspLeuSerSerGlnIle 397
Db      2496 AAATTCACCTCTCTGCGACAGATGCTGCTCTCTCTTGCATCAATATCCCAATC 2555
Qy      398 LysGlyCysLeuValThrAlaSerAlaAspLysTyrValLysIleThrAspLileLeuGly 417
Db      2556 CGCGGGTGTATCTTACTGCGGCGATGAGCAAAACGTCTCAAAATTTGGAAAGTCCAAAGAC 2615
Qy      418 AspArgPro-----SerLeuValHisSerArgAsp 427
Db      2616 GAGGAATCTGAAGATATCCCGCCCGCAGAGGAAATCAATCTTGCACCTCACAGAC 2675
Qy      428 MetLysMetGlyValLeuPheCysSerSerCysAspProAsp-----LeuProPheIle 445
Db      2676 CTGCGCTTGATGAGGCTTCGCGCGCCGATGACCTGATCCCGAGACCACTTACA 2735
Qy      446 TyrAlaPheGlyGlyGlnLysGluGlyLeuArgValIleThrAspLileSerThrValSerSer 465
Db      2736 GTTCCGCGACCCGTTACAAAGCACTTTCAGATGTGGAGCGTGGCTCCCAACCCCGGA 2795
Qy      466 ValAsnGluLapPheGlyArgArgGluArg 475
Db      2796 GCAAGAAAGCGTTCCGATGAGAGGCTGAGA 2825

RESULT 15
US-09-938-842A-2540
; Sequence 2540, Application US/0938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
```


Search completed: January 31, 2004, 04:36:00
job time : 530 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 31, 2004, 03:09:12 ; Search time 100 Seconds
(without alignments)
2211.329 Million cell updates/sec

Title: US-09-315-355C-10

Perfect score: 2640

Sequence: 1 MNRSROVTCVAVWRCVAKK.....RNSISGPFGRSSDTPMES 501

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=x1p
-Q=/cgn2_1/USFTO.spool/p/US09315355/runat.30012004.091905.24404/app.query.fasta.1.647
-DB=Issued_Patents_NA -OPMT=fastap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US09315355 @CNC 1.1.85 @runat.30012004.091905.24404 -NCPU=6 -ICPI=3
-NO_MMAP -IARSEOUTRY -NEG_SCORES=0 -WAIT -DSFBLCK=100 -LONCLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:

1: /cgn2_6/pctdata/2/ina/5A.COMB.seq:*
2: /cgn2_6/pctdata/2/ina/5B.COMB.seq:*
3: /cgn2_6/pctdata/2/ina/6A.COMB.seq:*
4: /cgn2_6/pctdata/2/ina/6B.COMB.seq:*
5: /cgn2_6/pctdata/2/ina/6C.COMB.seq:*
6: /cgn2_6/pctdata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	303.5	11.5	696	3	US-08-998-416-1050
2	216	8.2	2314	3	US-08-105-454-1
3	205.5	7.8	1929	3	US-08-105-454-9
4	200.5	7.6	1211	3	US-09-063-743-2
5	200.5	7.3	1211	4	US-09-560-540-2
6	191.5	7.3	2119	3	US-09-032-372-6
7	190.5	7.2	1738	4	US-09-620-312D-615
8	190.5	7.2	2100	4	US-09-013-118-2
9	179	6.8	274	4	US-09-313-284A-1839
10	179	6.8	2481	3	US-08-899-578-1
11	179	6.8	43676	3	US-09-356-952-12
12	178.5	6.8	1221	3	US-08-965-600-2

13	178.5	6.8	1221	4	US-09-489-506-2	Sequence 2, Appl1
14	178.5	6.8	2338	4	US-09-620-312D-411	Sequence 411, App
15	173.5	6.6	2272	4	US-09-108-857-1	Sequence 1, Appl1
16	170.5	6.5	1907	4	US-09-149-476-78	Sequence 78, Appl1
17	167.5	6.3	2237	4	US-08-914-999-7	Sequence 7, Appl1
18	167	6.3	2152	1	US-08-188-582-17	Sequence 17, Appl1
19	167	6.3	2152	1	US-08-446-715-17	Sequence 17, Appl1
20	165.5	6.3	2359	1	US-08-188-582-4	Sequence 4, Appl1
21	165.5	6.3	2359	1	US-08-646-715-1	Sequence 4, Appl1
22	165	6.2	1368	3	US-08-707-399E-1	Sequence 3, Appl1
23	164	6.2	2085	2	US-08-283-917-8	Sequence 8, Appl1
24	164	6.2	2085	2	US-08-961-716-8	Sequence 8, Appl1
25	160	6.1	1841	4	US-09-620-312D-636	Sequence 636, App
26	159	6.0	7518	4	US-09-620-312D-1051	Sequence 1051, App
27	159	6.0	1611	4	US-09-302-769-13	Sequence 13, Appl1
28	158	6.0	1517	3	US-09-180-783-1	Sequence 1, Appl1
29	156.5	5.9	1517	3	US-08-914-999-5	Sequence 5, Appl1
30	155.5	5.9	3465	4	US-09-620-312D-867	Sequence 867, App
31	155	5.9	1366	4	US-08-988-856B-1	Sequence 1, Appl1
32	154.5	5.9	1767	5	PCT-US95-01806-1	Sequence 1, Appl1
33	154.5	5.8	2363	4	US-09-620-312D-222	Sequence 222, App
34	153	5.8	1858	2	US-08-909-965C-11	Sequence 11, Appl1
35	151	5.7	3067	4	US-09-016-434-1285	Sequence 1285, App
36	150.5	5.7	1700	3	US-08-988-856B-3	Sequence 3, Appl1
37	149.5	5.7	1700	3	PCT-US95-01806-3	Sequence 3, Appl1
38	149.5	5.6	1563	3	US-09-177-249-3	Sequence 3, Appl1
39	147	5.6	1246	4	US-09-302-769-22	Sequence 22, Appl1
40	146.5	5.5	1394	3	US-09-147-826B-1	Sequence 1, Appl1
41	145.5	5.5	2186	4	US-09-184-001-3	Sequence 1, Appl1
42	145	5.5	2558	4	US-09-184-001-3	Sequence 3, Appl1
43	144.5	5.5	1115	1	US-08-190-802A-19	Sequence 19, Appl1
44	144.5	5.5	1115	3	US-08-477-346-19	Sequence 19, Appl1
45	144.5	5.5	1115	3	US-08-477-346-19	Sequence 19, Appl1

ALIGNMENTS

RESULT 1
US-08-998-416-1050
Sequence 1050, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jürgen
APPLICANT: Knechtle, Philipp
APPLICANT: Reibschung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CCG1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1050:
SEQUENCE CHARACTERISTICS:
LENGTH: 696 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1640UP
US-09-998-416-1050

Alignment Scores:
Pred. No.: 2,16e-24 Length: 696
Score: 303.50 Matches: 87
Percent Similarity: 45.88% Conservative: 30
Best Local Similarity: 34.12% Mismatches: 71
Query Match: 11.50% Indels: 68
DB: 3 Gaps: 8

US-09-315-355c-10 (1-501) x US-08-998-416-1050 (1-696)

Qy 31 GluValysArgLeuIleAlaGluAlaGlyGluLeuGluGluGluGluGlyGlySer 50
Db 8 GAGCTGGGGCGGCGCTGACGCTGACGATGCGGAGAGGCGCTGAGAGAGCGCGGTGGCG 67
Qy 51 AspGluGluGluThrGlySerProSerGluAspGlyMetGlnSerAlaArgThrGlnAla 70
Db 68 CAGAGGGCGCGGCGCTGGCGCGCAATTGACCGT----- 103
Qy 71 ArgProArgGluProLeuGluAspGlyAspProGluAspAspArgThrLeuAspAspAsp 90
Db 104 -----GACGAC 109
Qy 91 GluLeuAlaGluIleAspLeuAspLeuAspLeuAspLeuAspLeuAspLeuAspLeu 108
Db 110 GACCTGAAGAGAGTGGAGCTTGGAGACTACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 169
Qy 109 GluThrLeuGluGluSerLeuLeuGlyLeuThrValTyr-----GlySerAsnAspGln 126
Db 170 GTGACGATGTTCCGGGGCTCTCGGGCGAGCGGCGCTTCCAGAGGGGTGAGAGGGGAG 229
Qy 127 AspProIleValThrLeuLys-----AspThrGluGlnTyrGluValGluAspPheLeu 144
Db 230 GACCGTACCTGAGCTTCCCAACCGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 289
Qy 145 IleLysProSerAspAsnLeuIleValCysGlyArgAlaGluGluAspGlnCysAsnLeu 164
Db 290 GTGATCCCGACAGACACCTGCTGTGGCAACGGGACGAGACGACATTCTGACTCTG 349
Qy 165 GluValHisValTyrAsn----- 170
Db 350 GACGTGACGTGACGACGAGCGCGGGGTTCCACAGACGAGGGGGTCCCGACAGAGGCC 409
Qy 171 -----GluGluGluAsp-----SerPheTyrVal 178
Db 410 GGGGACGGCGAGACCCCGACGTGGCGCGCGCTGATACGAGACGCTCTTGTACCTG 469
Qy 179 HisHisAspIleLeuLeuSerAlaTyrProLeuSerValGluTyrLeuAsnPheAspPro 198
Db 470 CACACGACGTGATGTTCCGCACTTCCGCTGTGCGGAGAGAGAGAGAGAGAGAGAGAG 529
Qy 199 ---SerProAspAspSerThrGlyAsnTyrIleAlaValGlyAsnMetThrProValIle 217
Db 530 GGGGTGAACCTGACGCGCGCGGCAAACTTTCGGGGGTGCGGACCTTGCACCCACGATC 589
Qy 218 GluValTyrAspLeuAspIleValAspSerLeuGluProValPheThrLeuGly----- 235
Db 590 GAGCTGTGACACGTGCTGTGTGACCGCGCGCTCCGAC-ATGATCTCTGGGAGAGCCC 648

Qy 236 -----SerLysLeuSerLysLysLysLysLys 244
Db 649 GCGGACTGTGCGACCGCGTCCAAAGATCGAAGAGAGAGAGAGAGAGAGAGAGAGAG 693

RESULT 2
US-08-105-454-1
Sequence 1, Application US/08105454
Patent No. 6071715
GENERAL INFORMATION:
APPLICANT: Qian, Yue-Wei
TITLE OF INVENTION: No. 6071715el Proteins Which Bind to
TITLE OF INVENTION: Retinoblastoma Proteins and Their
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 2300 One American Center
CITY: Austin
STATE: TX
COUNTRY: USA
ZIP: 78701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,454
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kirchell, Barbara
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSK:196/KIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-474-7577
TELEFAX: 512-474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2314 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 85..1362
US-08-105-454-1

Alignment Scores:
Pred. No.: 7.9e-14 Length: 2314
Score: 216.00 Matches: 84
Percent Similarity: 35.97% Conservative: 66
Best Local Similarity: 20.14% Mismatches: 133
Query Match: 8.18% Indels: 134
DB: 3 Gaps: 13

US-09-315-355c-10 (1-501) x US-08-105-454-1 (1-2314)

Qy 81 ProGluAspAspArgThrLeuAspAspGluLeuAlaGluIleAspLeuAspLeuAspLeu 100
Db 343 CCTAATGATAT-----CCTCAGTTTATGCTGACACTAC 378
Qy 101 AspGluGluGluAspProAspAlaGluThrLeuGlyGluSerLeuLeuGluLeuThrVal 120
Db 379 GACAGTGAG-----AAAGAGAA-----TTTGAGGT 405
Qy 121 TyrGlySerAsnAspGluAspProIleValThrLeuLysAspThrGluGlnTyrGluArg 140
Db 406 TTGGTTCAGTTAGTGAGAAAAATTGAATTGAATCAACCATGAAGAGAGAGTA 465

```

QY 141 GluAspPheLeuIleLysProSerAspAsnLeuIleValCysGlyAlaGluGlnAsp 160
Db 466 AACAGGCGCCGTATATGCCCCAGAACCCCTTGATCATCGAACAAAGACCTCTTCAGT 525
QY 161 -----GlnCys 162
Db 526 GATGTTCTTGCTTGTACTATACAAAACATCCTTAAACAGATCCTTGTGAGAGAGC 585
QY 163 AsnLeuGluValHisValTyrAsnGlnGluAspSerPheTyrValHisAspIle 182
Db 586 AACCCAGACTGCGCTCCCGGACATCAGAAAGAGAGCTATGGCTTCTTGGAAACCA 645
QY 183 LeuLeuSerAlaTyrProLeuSerValGluTyrLeuAsnPheAspProSerProAsp 202
Db 646 AATCTCAGTGGGCACTTACTTAGT-----GTTTCAGATGAC 681
QY 203 SerThrGlyAsnTyrIleAlaValGlyAsnMetThrProValIleGluValTyrAspLeu 222
Db 682 CATACC-----ATCTGCGCTGGGACATC 705
QY 223 AspIleValAspSerLeuGluProValPheThrLeuGlySerLysLeuSerLysLys 242
Db 706 AGTGCCGTT----- 714
QY 243 LysLysLysGlyLys-----LysSerSerSerAlaGluGlyHisThrAspAlaVal 259
Db 715 CCAAGAGAGGAGAAAGGTAGATCCGAAAGCAATCTTACAGGCAATACGAGTGA 774
QY 260 LeuAspLeuSerTyrPheAsnLysLeuIleArgAsnValLeuAlaSerAlaSerAlaAsp 279
Db 775 GAATATGTTCTCGCATCTACTCATGATGATGCTGTTGGGTCAATGTCAGATGATCAG 834
QY 280 ThrValIleLeuTyrAspMet-----SerLeuGlyLysProAlaIleSerLeuAla 296
Db 835 AAACCTTAGATTTGGGATCTCGTTCAACAACATCTTCAACCAAGCCACTCGATTAT 894
QY 297 ValHisThrAspLysValGlnThrLeuGlnPheHisProPheGluAlaGlnThrLeuIle 316
Db 895 GCTCACAATGCGTAAGTACGCGCTTCTTCAATCTTATAGAGATTCAATCTTCC 954
QY 317 SerGlySerTyrAspLysSerValAlaLeuTyrAspCysValGserProAspGluSerHis 336
Db 955 ACAGATGATCGTCAAGACTGCTGCTGTCGAGTCAAG----- 996
QY 337 ArgMetTyrArgPheSerGlyGlnIleGluArgValThrTyrAsnHisPheSerProCys 356
Db 996 ----- 996
QY 357 HisPheLeuAlaSerThrAspAspGlyPheValTyrAsnLeuAspAlaArgSerAspLys 376
Db 997 -----AATCGAAACTTAG----- 1011
QY 377 ProIlePheThrLeuAsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSerSerGln 396
Db 1012 ---TTGCAATCTCTTGATGACATATAGATGAATATTCAGAGTTCACTGATCACCCTCAC 1068
QY 397 IleLysGlyCysLeuValThrAlaSerAlaAspLysTyrValLysIleTyrAspIle--- 415
Db 1069 AATGAGACTATTTTGTCTTCCAGTCTACTGTCCAGACTGATGATGTGGATTTTAGT 1128
QY 416 ---LeuGlyAspArgProSerLeuValHisSerAlaGlyAspMetLysMetGlyValLeuPhe 434
Db 1129 AAAATTTGAGAGAACATTCCTCCAGAAATGACAAAGAGGAGCCACAGAGTTGTTT 1188
QY 435 CysSer-----SerCysCysProAspLeuProPhe 444
Db 1189 ATTCATGTCATCTACTGCAAGATATCTGATTTCTCTGGAATCCCAATGAACCTTGG 1248
QY 445 IleTyrAlaPheGlyGlyGlnLysGluValLeuArgValTyrAspIleSer 461
Db 1249 GTGATTTGTTCTGTATCAGAAAGCAATATCATGCAAGTGTGGCAATGGCA 1299

```

```

US-08-105-454-9
; Sequence 9, Application US/08105454
; Patent No. 6071715
; GENERAL INFORMATION:
; APPLICANT: Qian, Yue-Wei
; APPLICANT: Lee, Eva Y.-H. P.
; TITLE OF INVENTION: No. 6071715el Proteins which Bind to
; TITLE OF INVENTION: Retinoblastoma Proteins and Their
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 2300 One American Center
; CITY: Austin
; STATE: TX
; COUNTRY: USA
; ZIP: 78701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/105,454
; FILING DATE: Concurrently herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: USK:196/KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1929 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-105-454-9
;
; Alignment Scores:
; Pred. No.: 8.68e-13 Length: 1929
; Score: 205.50 Matches: 71
; Percent Similarity: 38.36% Conservative: 69
; Best Local Similarity: 19.45% Mismatches: 102
; Query Match: 7.78% Indels: 123
; Gaps: 12
;
; US-09-315-355c-10 (1-501) x US-08-105-454-9 (1-1929)
QY 126 GlnAspProGlyValThrLeuLysAspThrGluGlnTyrGluArgGluAspPheLeuIle 145
Db 661 CAGAACTCCTCAATCATCTGCTACAAAACA----- 690
QY 146 LysProSerAsnLeuIleValCysGlyArgAlaGlu----- 158
Db 691 ---CCATCTTCTGATGGTGGTGGTTTGTACTATACAAAACCCCTGTAACAGACCCA 747
QY 159 GlnAspGlnCysAsnLeuGluValHisValTyrAsnGlnGluAspSerPheTyrVal 178
Db 748 AGTGAAGAAATATATCTGATCTCAGATTAAAGAGTCAACAGAAAGAGAGCTATGCTC 807
QY 179 HisHisAspIleLeuLeuSerAlaTyrProLeuSerValGluTyrLeuAsnPheAspPro 198
Db 808 TCTCGAATTCAAATTTGAGTGGACATCTCTTAAGT----- 843
QY 199 SerProAspAspSerThrGlyAsnTyrIleAlaValGlyAsnMetThrProValIleGlu 218
Db 844 GCATCTATATGACCATCT-----GTTTGT 867
QY 219 ValTyrAspLeuAsp-----IleValAspSerLeuGluProVal 231

```

```

      868 CTGTCGATATTAACGACAGCAAAAGACGCAAAATTTGGATGCT---AAAGCATC 924
      232 PheThrLeuGlySerLysLeuSerLysLysLysLysLysLysLysLysSerSerSer 251
      925 TTTACT----- 930
      252 AlaGluGlyHisThrAspAlaValLeuAspLeuSerThrPheLysLeuLeuArgAsnVal 271
      931 -----GGCCACTACAGCTGTTGTAGAGGATGTCGCTGGACCTGCACAGTGCATG 984
      272 LeuAlaSerAlaSerAlaAspAsnThrValLeuLeuThrPheMet-----SerLeu 288
      985 TTTGGATCTGTTGGTGTGATGACAGAACTATGATGATGGACACACAGTCCATACACACC 1044
      289 GlyLysProAlaAlaSerLeuAlaValHisThrAspLysValGlnThrLeuGlnPheHis 308
      1045 TCCAAAGCCGAGCTCACTTGTGATGCGCACACTGCCAGATCAACTGCTCTCATTTCAAT 1104
      309 ProPheGluAlaGlnThrLeuLysSerGlySerLysLysSerValAlaLeuThrAsp 328
      1105 CCTACAGCGAATTTATTTCTAGCCACCGGCTCTGGGATTAAGACCGTATGCTTATGGAT 1164
      329 CysArgSerProAspGluSerHisArgMetTrpArgPheSerGlyGlnLeuArgVal 348
      1165 CTGGCT----- 1170
      349 ThrTrpAsnHisPheSerProCysHisPheLeuAlaSerThrAspArgLysPheValTyr 368
      1170 ----- 1170
      369 AsnLeuAspAlaArgSerAspLysProIlePheThrLeuAsnAlaHisAsnAspGluIle 388
      1171 AACTTAAATTAATAA-----CTCATACCTTCGAATCTCGAATTAAGATGAATTT 1218
      389 SerGlyLeuAspLeuSerSerGlnIleLysGlyCysLeuValThrAlaSerAlaAspLys 408
      1219 TTCACAGTCCACTGCTCTCCACATTAATGAATACTATTCGCTCAAGGTACTGACCGC 1278
      409 TyrValLysIleThrPhePheIle-----LeuGlyAspArgProSerLeuValHisSerArg 426
      1279 CGCCTGAATGTGTGGATTAAGTAAATTTGGAGAAACAATCAACGACGAAAGATGCA 1338
      427 AspMetLysMetGlyValLeuPheCysSer----- 436
      1339 GATGGCGCTCCAGAACTCTCTTTATTCATGAGAGACACACTGCTAAGATTTCAGATTTT 1398
      437 SerCysCysProAspLeuProPheIleTyrAlaPheGlyGlyGlnLysGlyLysLeuArg 456
      1399 AGCTGGAACCCCAATGAGCCTTGGGTTCATTTGCTCAGTGTCTGAGGATTAACATCATG 1458
      457 ValTrpAspIleSer 461
      1459 ATATGGCAATATGGCT 1473

```

RESULT 4

```

US-09-063-743-2
Sequence 2, Application US/09063743
Patent No. 6242214
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: HUMAN GTPASE-ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA

```

```

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/063,743
CLASSIFICATION:
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0508 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1211 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGNOR01
CLONE: 059953
US-09-063-743-2

```

Alignment Scores:

```

Pred. No.: 1,48e-12 Length: 1211
Score: 200.50 Matches: 82
Percent Similarity: 43.56% Conservative: 60
Best Local Similarity: 25.15% Mismatches: 129
Query Match: 7.59% Indels: 55
DB: Gaps: 13

```

US-09-315-355c-10 (1-501) x US-09-063-743-2 (1-1211)

```

      182 ILeuLeuSerAlaTyrProLeuSerValGluTyrLeuAsnPheAspProSerProAsp 201
      229 ATCTGCTCTCGAATGAAGGGAAGGCTTACTGCTCAAGTCCACCCCAAC----- 282
      202 AspSerThrGlyAsnTyrIleAlaValGlyAsnMetThrProValIleGluValTrpAsp 221
      283 -----GGATCCACCTTAGCATCTGCAGATTGACCGCACTGATATTACTGTG--- 330
      222 LeuAspIleValAspSerLeuGluProValPheThrLeuGlySerLysLeuSerLysLys 241
      331 ---AATGCTATATGCTGACTGTGATTAATCATGCCACACTG----- 366
      242 LysLysLysLysGlyLysLysSerSerSerAlaGluGlyHisThrAspAlaValLeuAsp 261
      367 -----AAGGACACACGTGAGAGATGAA 393
      262 LeuSerTrpAsnLysLeuIleArgAsnValLeuAlaSerAlaSerAlaAspAsnThrVal 281
      394 TTGCATTACAAAC---ACAGATGGCAGTATGCTTTTCTTCAGCACTCCACAGTAAACCGTG 450
      282 IleLeuTrpAspMetSerLeuGlyLysProAlaAlaSerLeuAlaValHisThrAspLys 301
      451 GCTGTGTGGATAGTGAACAGGTGAGGCTTAAAGCTTAAAGGACATTACTTCTTT 510
      302 ValGlnThrLeuGlnPheHisProPheGluAlaGlnThrLeuLysSerGlySerLysAsp 321
      511 GTGAATTCCTGTTATCCAGCAGAGAGAGGCCCTCAGCTGTCTGCACTGGCAGTACGAT 570
      322 LysSerValAlaLeuTyrAspCysArgSerProAspGluSerHisArgMetTrpArgPhe 341
      571 GGCACAGGTAAAGCTTTGGGACATCCGGAAG---AAAGCAGCCATTCAGACATTTCAAGAC 627

```

QY 342 SerGlyGlnIleGluArgValThrTrpAsnHisPheSerProCysHisPheLeuAlaSer 361
DB 628 ACATACAGAGGTGTTAGCTGATGACCTTCAATGACACAGATGAT---CAGATTATTTCTGGT 684
QY 362 ThrAspArgGlyPheValTyrAsnLeuAspAlaArgSerAspGlyProIlePheThrLeu 381
DB 685 GGAATTAACATGATGATTCAGATGCTGGGACCTGGCCAGAACAGCTTAACCTACACCATG 744
QY 382 AsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSerSerGlnIleGlyCysLeu 401
DB 745 AGAGCCATGACATTCAGTACGACCTGCTGATTAACTTGA---GGCTTTATCTT 801
QY 402 ValThrAlaSerAlaAspLysTyrValLysIleTrpAspIleLeuGlyAspArgProSer 421
DB 802 TTGTCCATGCAATGACAAATACAGTTGCTGTGGATGTC-----CGGCATTT 852
QY 422 LeuValHisSerAlaGAspMetLysMet-----Gly 431
DB 853 GCCCCCAAGAGATGTGTAAAGATATTTCAAGAGAAATGTCACAACTTTGAAAGAAC 912
QY 432 ValLeuPheCysSerSerCysCysProAspLeuProPheIleTyrAlaPheGlyGln 451
DB 913 CTTCCTGAGATG---TCTTGCTCACCTGATGGAACAAATA---GACGCTGCTCAGCC 966
QY 452 LysGluGlyLeuArgValTrpAspIleSerThr----- 462
DB 967 GACAGGTTTGTATTGTTGTGGATACCAACAGCAGAGAAATATTGTAAGCTGCCGCC 1026
QY 463 ---ValSerSerValAsnGlu---AlaPheGlyArgGluArgGlyLeuValLeuGlySer 480
DB 1027 CATGCTGCTCCATCAATGAAGTGGCTTTCCACCCTGATGAGCCATCATATTATCTCAGCA 1086
QY 481 AlaArgAsnSerSerIle 486
DB 1087 TCGAGTACAGAGACTG 1104

RESULT 5
US-09-590-540-2
Sequence 2, Application US/09590540
Patent No. 6410267
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Lal, Preeti
Guegler, Neil J.
Patterson, Chandra
TITLE OF INVENTION: HUMAN GTPASE-ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Genomics, Inc.
STREET: 3160 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 3.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/590,540
FILING DATE: 08-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/063,743
FILING DATE: April 21, 1998
ATTORNEY/AGENT INFORMATION:
NAME: David G. Streeter
REGISTRATION NUMBER: 43,168
REFERENCE/DOCKET NUMBER: PF-0508-1 DIV
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1211 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGNOT01
CLONE: 059953
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-590-540-2
Alignment Scores:
Score: 1.48e-12 Length: 1211
Percent Similarity: 200.50 Matches: 82
Best Local Similarity: 43.56% Conservative: 60
Query Match: 7.59% Mismatches: 129
DB: 4 Indels: 55
Gaps: 13
US-09-315-355c-10 (1-501) x US-09-590-540-2 (1-1211)
QY 182 IleLeuLeuSerAlaTyrProLeuSerValGluTrpLeuAsnPheAspProSerProAsp 201
DB 229 ATGCTGCTCTCTGACATGAAGGAGAGTCTACTGCGCAAGTCCACCCCAAC----- 282
QY 202 AspSerThrGlyAsnTyrIleAlaValGlyAsnMetThrProValIleGluValTrpAsp 221
DB 283 -----GGATCCACTTACATGATCTGCAGAGATTGACGACATGATTAATCTGTG--- 330
QY 222 LeuAspIleValAspSerLeuGluProValPheThrLeuGlySerLysLeuSerLysLys 241
DB 331 ---AATGCTATGAGTGACTGTGATTAATGACACTG----- 366
QY 242 LysLysLysLysGlyLysLysSerSerSerAlaGluGlyHisThrAspAlaValLeuAsp 261
DB 367 -----AAGGACACAGCTGAGCATGATGAA 393
QY 262 LeuSerTrpAsnLysLeuIleArgAsnValLeuAlaSerAlaAspAsnThrVal 281
DB 394 TTGCATTACAAAC---ACAGATGGCAGATGCTTTCTCAGATCCACAGATTAACCGCTG 450
QY 282 IleLeuTrpAspMetSerLeuGlyLysProAlaAlaSerLeuAlaValHisThrAspLys 301
DB 451 GCTGTGTGGATGATGGAACAGGTGAAGGGTTAAAGGCTAAAGGACATACTTCCTT 510
QY 302 ValGlnThrLeuGlnPheHisProPheGluAlaGlnThrLeuIleSerGlySerTyrAsp 321
DB 511 GTGAATTCCTGTTATCCAGCCAGAGAGCCCTGACTGTCTGACATGCGAGATGAT 570
QY 322 LysSerValAlaLeuTyrAspCysArgSerProAspLeuSerHisArgMetTyrArgPhe 341
DB 571 GGCACAGGTAAAGCTTTGGAGATCCGGAAG---AAACAGACCATCCAGACATTTCAGAAC 627
QY 342 SerGlyGlnIleGluArgValThrTrpAsnHisPheSerProCysHisPheLeuAlaSer 361
DB 628 ACATACAGAGGTGTTAGCTGATGACCTTCAATGACACAGATGAT---CAGATTATTTCTGGT 684
QY 362 ThrAspArgGlyPheValTyrAsnLeuAspAlaArgSerAspGlyProIlePheThrLeu 381
DB 685 GGAATTAACATGATGATTCAGATGCTGGGACCTGGCCAGAACAGCTTAACCTACACCATG 744
QY 382 AsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSerSerGlnIleGlyCysLeu 401
DB 745 AGAGCCATGACATTCAGTACGACCTGCTGATTAACTTGA---GGCTTTATCTT 801
QY 402 ValThrAlaSerAlaAspLysTyrValLysIleTrpAspIleLeuGlyAspArgProSer 421
DB 802 TTGTCCATGCAATGACAAATACAGTTGCTGTGGATGTC-----CGGCATTT 852


```

Db      874 -TCGGCGACGTCGTCGAGCGCTTTGAAACACATGAATCGACATCAACAGTCGCGTA 932
Qy      358 -----PheleuAlaserThrAspAspGlyPheValTyraAsnLeuAs 371
Db      933 CTACCCCGAGTGAAGATGCTTTGCTTCAAGGTCAGATCGTACGTGCGCTTATGGA 992
Qy      371 PALATGSeSerAspLysProIlePheThrLeuAsnAlaHisAsnAspGluIleSerGlyLe 391
Db      993 CTGCGGGCGAGATAGGAGGTTGCCATCTATTCAAAAGAAAGCATATTTGGAGATC 1052
Qy      391 uAspLeuSerSerGlnIleLysGlyCysLeuValThrAlaSerAlaAspLysTyr--Va 410
Db      1053 CACGCTGCAGCTTCTCCCTCAGTGGTCGCTGCTGCTTTGGATACATATTAACATAT 1112
Qy      410 LysIleThrAspIleLeu---GlyAspArgProSerLeuValHisSerArgAspMetLys 429
Db      1113 CAACGTCGTGGATGTTCTCAAAAGGTCGCCGCTGCTTGGATGACATGAACAAACCG 1172
Qy      429 smet-----GlyValLeuPheCysSerSerCysCysProAs 441
Db      1173 CGTTAGACACTCTAGACTTTCCCGCATGGAGCTGCTTCTGCTCT----- 1218
Qy      441 pleuProPheIleTyrAlaPheGlyGlyGlnLysGlyLeuArgValIleAspIleSe 461
Db      1219 -----GGATCATGGAGATCATACCTCAGAGTCTGGGCGCTAATC 1256
Qy      461 rThrValSerSer 465
Db      1257 ATCTTCTGACAGT 1269

```

RESULT 7

```

US-09-620-312D-615
; Sequence 615, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jianshui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungding
; APPLICANT: Wang, Dunru
; APPLICANT: John Tillinghast
; APPLICANT: Dimanac, Radoje T.
; TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pc_fl_genes Version 1.0
; SEQ ID NO 615
; LENGTH: 1738
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (196)..(1467)
; US-09-620-312D-615

```

```

Alignment Scores:
Pred. No.: 3,42e-11 Length: 1738
Score: 190.50 Matches: 91
Percent Similarity: 34.52% Conservative: 55
Best Local Similarity: 21.51% Mismatches: 138
Query Match: 7.22% Indels: 139
DB: 4 Gaps: 17

```

US-09-315-355c-10 (1-501) x US-09-620-312D-615 (1-1738)

```

Qy      132 LeuLysAspThrGlnIleTyrGluArgGlu-----AspPheLeuIleLys----- 146
Db      316 CTAAAGACAAATAATAGTTCCACAAACATGTGAGATTGATTTCTTTATTAAGGCCAG 375
Qy      147 -----ProSerAspLeuIleValIleCysGlyArgGluGlnAspGlnCys 162
Db      376 TTTCGCGAATGCCCTTGGACAAA-----CACATGAAATGGAGAACATC 420
Qy      163 AsnLeuGlu-----ValHisValTyrAsnGlnGlnAspSer 175
Db      421 TCATCAGAAAGAGTGTGAAATAGAAATAGTGGAGAGATATCTGCACCCGACGAG 480
Qy      176 PheTyrValHisAspIleLeuLeuSerAlaTyrProLeuSerValGluThrPheAsn 195
Db      481 CAATGCATCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 534
Qy      196 PheAspProSerProAspSerThrGlyAsnTyrIleAlaValGlyAsnMetThrPro 215
Db      535 -----ATCTGACTGCTGCTTATGATAG 558
Qy      216 ValIleGluValIleAspLeuAspIleValAlaSerLeuGluProValPheThrLeuGly 235
Db      559 ACTTCGCGATCGTCGCTTGGAA----- 582
Qy      236 SerLysLeuSerLysLysLysLysLysGlyLysLysSerSerAlaGlnGlyHis 255
Db      583 -----GGAAGATCATATATGACAAATGTCGAGCAT 612
Qy      256 ThrAspAlaValLeuAspLeuSerThrAsnLys-----LeuIleArgAsnValLeuAla 273
Db      613 ACGGATGTTGTAATAAGATGCGCTGGTCAAAAAGATAGTTGTCCTGCTTATATTTG 672
Qy      274 SerAlaSerAlaAspSerThrValIleLeuThrAspMetSerLeuGlyLysProAlaAla 293
Db      673 AGTCCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 714
Qy      294 SerLeuAlaValHisThrAspLysValGlnThrLeu-----GlnPheHisProPhe 310
Db      715 -----GTAGAGAGAAACAAAGTAAAGCCCTACACTGCTGTAGAGGTGATGGA 765
Qy      311 GluAlaGlnThrLeu-----IleSerGlySerTyrAsp 321
Db      766 AGTGTAGATTCTATACCTGTTGATGCTCAGAACTAAATTTCGAGTGGCTCTGGAT 825
Qy      322 LysSerValAlaLeuTyrAspCysArgSerProAspGlnSerHisArgMetThrArgPhe 341
Db      826 AAGATGCTAAAGATCTGCTGATACAGTCCCTACAGATGAAGAATAATAAG----- 876
Qy      342 SerGlyGlnIleGluArgValThrTyrAsnHisPheSerProCysHisPheLeuAlaSer 361
Db      877 -----CAGAGTCCACA----- 888
Qy      362 ThrAspAspGlyPheValTyrAsnLeuAspAlaArgSerAspLys----- 376
Db      889 -----AATCGACCAAGAAAGAAACAGAGACAGAAACAGTTGGGA 927
Qy      377 -----ProIlePheThrLeuAsnAlaHisAsnAspGluIleSerGlyLeuAsp 392
Db      928 CTAAACAAGACTCCATAGTACCTCTCTGCGCAACATGAGGCACTTCTCAGTTCTG 987
Qy      393 LeuSerSerGlnIleLysGlyCysLeuValThrAlaSerAlaAspLysTyrValLysIle 412
Db      988 TGGTCAGATCTGAAAGAAATCTGC-----AGTGCATCTTGGAGCATACATTAAGATG 1041

```

QY 413 TrpAspIleLeuGlyAspArgProSerIleuValHisSerArgAspMetLysMetGlyVal 432
|||
Db 1042 TGGATGTGAGTGTGGCAGCTTAAGTCACACTTGGACAGAAATAAGTTTAATGT 1101
QY 433 LeuPheCysSerSerCysCysProAspIleuProHeIleTyralaPheGlyGlnLys 452
|||
Db 1102 ATTCTTATCTCTCCACTTTGTAACGTTTA-----GCATCTGGAAAGCAGAT 1149
QY 453 GluIleuArgValTrpAspIleSerThr----- 462
|||
Db 1150 AGGCATATCAGACTGTGGATCCCGAAGCTAAAGATGTTCTTGGTGTGCTGCTCCCTA 1209
QY 463 -----ValSerSerValaGlnIlePheGlyArgGluArgLeu 476
|||
Db 1210 ACGTCACATCTGGTGGTGACATCAGTAATAAGTCTCTACCCATGAAACAGACAGTG 1269
QY 477 ValLeuGlySerAlaArgAspSerIleSerGlyProPheGlySerArgSerAsp 496
|||
Db 1270 ATTTCAGATCTTTAGATTAAC-----ATTGTTAAGCTGTGGATACAGAAAGTTGTAG 1323
QY 497 ThrProMet 499
|||
Db 1324 GCTCTCTC 1332

RESULT 8

US-09-013-118-2

Sequence 2, Application US/09013118

Patent No. 6503708

GENERAL INFORMATION:

APPLICANT: Lal, Preeti

APPLICANT: Corley, Neil C.

TITLE OF INVENTION: MICROTUBULE-ASSOCIATED PR

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Dr.

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

FILING DATE: Filed Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PR-0464 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2100 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: BLADTUT02

CLONE: 1312429

US-09-013-118-2

Alignment Scores:

	Pred. No.:	4,63e-11	Length:	2100
	Score:	190.50	Matches:	91
	Percent Similarity:	34.52%	Conservative:	55
	Best Local Similarity:	21.51%	Mismatches:	138
	Query Match:	7.22%	Indels:	139
	DB:	4	Gaps:	17
US-09-315-355c-10 (1-501) x US-09-013-118-2 (1-2100)				
QY 132 LeuLysAspThrGlnGlnTyrgluArgGlu-----AspPheLeuIleLys----- 146				
Db 319 CTAAAGACAAAATGATGCTTCCACAAACATGTGAGATTATTTCTTATTAAAGGCCAG 378				
QY 147 -----ProSerAspAsnLeuIleValCysGlyArgAlaGlnIleAspGlnCys 162				
Db 379 TTTCTGGCAATGCCCTTGACAAA-----CACATGAAATGAGAAACGTC 423				
QY 163 AsnLeuGlu-----ValHisValTyrglnGlnIleAspSer 175				
Db 424 TCATCAGAAAGATTGTGAAATAGAAATACGTGAGAGAAATATCTGCACCCAGCCAGAG 483				
QY 176 PheTyrglnHisAspIleLeuLeuSerAlaTyrglnLeuSerValGluTrpLeuAsn 195				
Db 484 CAATGATGTTCCATGATGACGTGATCATTCAATTAAAGGCGAGAGAAATG----- 537				
QY 196 PheAspProSerProAspAspSerThrGlyAsnTyrlleAlaValAlaGlyAsnMetThrPro 215				
Db 538 -----ATCTTGACTGGTCTTATGATAG 561				
QY 216 ValIleGluValTrpAspLeuAspIleValAspSerLeuGluProValPheThrLeuGly 235				
Db 562 ACTTCTGGATCTGCTCTTGAA----- 585				
QY 236 SerLysLeuSerLysLysLysLysLysGlyLysLysSerSerSerAlaGlnLysHis 255				
Db 586 -----GAAAGCAATTAATGACAAATTTGGGACAT 615				
QY 256 ThrAspAlaValLeuAspLeuSerTrpAsnLys-----LeuIleArgAsnValLeuAla 273				
Db 616 ACGGATGTTTAAAGATGAGTGGCTGGTGAATAAAGATGTTGTCTGCTTATTATTG 675				
QY 274 SerAlaSerAlaAspAsnThrValIleLeuTrpAspMetSerLeuGlyLysProAlaAla 293				
Db 676 AGTCTTCTTATGATCAGACTATTTCTTATGGAGTGAAT----- 717				
QY 294 SerLeuAlaValHisThrAspLysValGlnThrLeu-----GlnPheHisProPhe 310				
Db 718 -----GTAGAGAGAAACAAAGTAAAGCCCTACACTGCTGTAGAGTCAATCTGGA 768				
QY 311 GluAlaGlnThrLeu-----IleSerGlySerTyrgAsp 321				
Db 769 AGTGTAGATTCTTATAGCTGTGATGCTGCTCAGAACTAAATTTTGCAGTGGCTCTG 828				
QY 322 LysSerValAlaLeuTyrgAspCysArgSerProAspGluSerHisValGluMetTrpArgPhe 341				
Db 829 AAGATGCTTAAAGATCTGCTGTACAGTCCCTACAGATTAAGAAGATGAAG----- 879				
QY 342 SerGlyGlnIleGluArgValThrTrpAsnHisPheSerProCysHisPheLeuAlaSer 361				
Db 880 -----GAGGAGTCCACA----- 891				
QY 362 ThrAspAspGlyPheValTyrglnLeuAspAlaArgSerAspLys----- 376				
Db 892 -----AATCGACCAAGAAAGAAACAGAAACAGAAACAGTTGGGA 930				
QY 377 -----ProIlePheThrLeuAsnAlaHisAsnAspGluIleSerGlyLeuAsp 392				
Db 931 CTAAACAGACTCCCATAGTACCCCTCTGGCCACATGAGGACGATTTCTTCAGTTCTG 990				
QY 393 LeuSerSerGlnIleLysGlyCysLeuValThrAlaSerAlaAspLysTyrgValLysAlle 412				
Db 991 TGTTCAGATGCTGAAGAAATCTGC-----AGTCGATCTTGGACCATACATTAAGAGTG 1044				

Oy	217	eglvatlrpaprleuaprllevalaspserleuclupovalpethrleuglyserly	237
	1050	AAACTTGG-----ACTACTGTGAT-----	1071
Oy	237	sleuserlyslslyslslysglylyslserserseralagllyhithras	257
Db	1072	-----GGTTCACTTCTTCATCACTTCAAGGACATTACTTC	1106
Oy	257	palvalleuapleuserltpaslyleuileargsnvalleuualaserlaaserla	277
Db	1107	CAGTTTGATGATGATGCT-----ATGGCTGGTTCATTACTTGCATCGATCAG	1157
Oy	277	aasphenthrvalilleutlrpasmetserleuglylspronalaaaserleuava	297
Db	1158	AGATACCACTCTCTCGTATGGAGCGTGAATCCGAGCTGACCTGGCACTTATCATCG	1217
Oy	297	lhithraslyslvalglnthrleuglnphehispropheglualaglnthrleuse	317
Db	1218	CCATCATCACCGCTTCATGCGTTCAA-----TTCAATGGAACAACGTGTGTTTC	1268
Oy	317	rglyserlyrpslysservalalaileutlyrpsrpsrarserserproasgluserhlsar	337
Db	1269	GGGAGGATATGATTTTACCCTTAATAT-----	1296
Oy	337	gmectlrpgrpheserlyglnlleugluargvalthrtprasnhipheserprocyshl	357
Db	1297	-----TGAAT-----	1302
Oy	357	sphleuualaserthrpsaspglyphevaltyrasleuapalaargerspyspr	377
Db	1303	-----GCTCACTGAGGATG	1319
Oy	377	olphehrleuansalahlaspasglulleserlyleuapleuserserglnl	397
Db	1320	TATCCGTACTCTGACCGGCTATTAATAAGATTATTTCTTCTCTTGAAGGAGC--	1377
Oy	397	elyserlycysevalthralaserlaasplyserlyvallyslterpaap-----	414
Db	1378	CGATCGATCGTGTCTGTGGTCTCTGAGACATTCATTCGCGTGGATTTTACAG	1436
Oy	415	-----laleuglyasprproserleuvalhlsersar	426
Db	1437	ACCGAAGCCAGAAATGTGTCTTTTGGAAAGACACCTCATCTTATCCGGAAT	1496
Oy	426	gaspmetrlysmetglyvalleuphecysserserocyssproaspleuprophelely	446
Db	1497	GCAATTCGAGGCAATATTTCTGTG-----TCATGCATGCAGAT-----	1536
Oy	446	ralapheglyglnlysgllyleuargvaltrpaspleserthrvalserSerVa	466
Db	1537	-----AGCGATGTAAAGTATGGATATTTCAGAGGAACTTGTGT	1577
Oy	466	lasnglualapheglyargargluargleu	476
Db	1578	ACACATGCTTCTGACATCGATCCGCTATC	1608
RESULT 11			
US-09-355-952-12			
Sequence 12, Application US/09356952			
Patent No. 6117663			
GENERAL INFORMATION:			
APPLICANT: Borlack-Sjodin, Ann			
APPLICANT: Margalit, S. M.			
APPLICANT: Bor-Sogli, Dafna			
APPLICANT: Cole, Philip			
APPLICANT: Kuxiyan, John			
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE			
TITLE OF INVENTION: THEREOF			
FILE REFERENCE: 600-1-228N			
CURRENT APPLICATION NUMBER: US/09/356,952			
CURRENT FILING DATE: 1999-07-19			
EARLIER APPLICATION NUMBER: 60/093,631			

		EARLIER FILING DATE: 1998-07-21	
		NUMBER OF SEQ ID NOS: 14	
		SOFTWARE: PatentIn Ver. 2.0	
		SEQ ID NO 12	
		LENGTH: 43676	
		TYPE: DNA	
		ORGANISM: Saccharomyces cerevisiae	
		US-09-356-952-12	
Alignment Scores:			
Pred. No.:	1.12e-07	Length:	43676
Score:	179.00	Matches:	75
Percent Similarity:	40.54%	Conservative:	60
Best local Similarity:	22.52%	Mismatches:	129
Query Match:	6.78%	Indels:	69
DB:	3	Gaps:	14
US-09-315-355C-10 (1-501) x US-09-356-952-12 (1-43676)			
Qy	167	HisValTyr--AamGlnGluLysAspSerPheTyrValHisHisAspIleLeuLeuSerAl	186
Db	16478	CAAGTCTACAGAGAAGAAATTGTTCCCTTTAAAGCGCAATTAGCACTGTTACTGCT--	16535
Qy	186	aTyProLeuSerValGluTyrLeuAsnPhe--AspProSerProAspAspSerThrGl	205
Db	16536	-----CTTTGGTGTACACAGCGCTCGTTTCATGACAAAGAGCCAGATTGAAGAGCA	16588
Qy	205	yaenTyrlleAlaValGlyAsnMetThrProValIleGluValTyrAspLeuAspIleVal	225
Db	16589	AAATTTTATGTATCTTGGCAGTGTACAAAACCTGCACGATATGCTCAATTAAATCTTGA	16648
Qy	225	laapSerLeuGluProValPheThrLeuGlySerLysLeuSerLysLysValyLysLys	245
Db	16649	TGAT-----TACTCAATAAAACTCCAGTCA	16675
Qy	245	sgLysLysSerSerSerSerAlaGluGlyHisThrAspAlaValLeuAspLeuSerTyrAs	265
Db	16676	TAAAGACTCCGTTACTACAGAGAACT-----	16703
Qy	265	nLysLeuIleArg-----	269
Db	16704	-----TTGATTCGTAATTTCAGCGTGAATCTGCATTTCAAGGTATTCGATTCGCACAGAGA	16759
Qy	270	----AsnValLeuAlaSerLysAserLysAspAsnThrValIleLeuTyrAspMetSerIle	288
Db	16760	AAATCCACGCTTGGCCACAGGTGGGCC-----AAGATTCATCTTTGGAGCGTTAACG	16813
Qy	288	uGlyLysProAlaAlaSerLeuAlaValHisThrAspLysValGlnThrLeuGlnPheHis	308
Db	16814	ATTGAAACCCAGTTTCCGATCTATCATCGGGAGCAGACAAACATTACTGTTAAATTCCA	16873
Qy	308	sProPheGluAlaGlnThrLeuIleSerGlySerTyrAspLysSerValAlaLeuTyrAs	328
Db	16874	TCAAAATGAAGACGATATCTGGCCAGTACTGGTAGTGAATTAATTGATGTTCTTACGA	16933
Qy	328	pCyAspSerProAspGlnSerHisArgMetTyrAspPheSerGlyGlnIleGluArgVal	348
Db	16934	CTTGAGAACCACTCCGCCACAAAGAAATTGTTCA--ACAAATGAGACCAATGCTAT	16990
Qy	348	lTnTTrAsnHisPheSerProCysHisPheLeuAlaSerTyrAspAspGlyPheValTyr	368
Db	16991	TTCGTGGAATCCATGAGAGCCCTTCAACTTTGTACTGCGCAATGAAGATCATAGAGCCCTA	17052
Qy	368	rAsnLeuAspAlaArgSerAspLysProIlePheThrLeuAsnAlaHisAsnAspGluIle	388
Db	17051	CTATTATGATATGAGGAATTTATCACT-----TCATTGAATGTATTCAAAGATCACTAGT	17104
Qy	388	eSerGlyLysLeuAspLeuSerGlnIleLysGlyCysLeuValThrAlaSerAl	406
Db	17105	CACCGCAGTATGATGAGTTCATTTCTCTCAACGGGGAGATGAGATGTATACGCTGCTGTA	17166
Qy	406	aAspLysTyrValLysIleTyrAspIleLeuGlyAspArgProSerLeuValHisSerArg	426

Mon Feb 2 10:52:38 2004

us-09-315-355c-10.p2n.rn1

Page 11.

Db 17165 CGATTAGAGTATCAGATATAT-----AAGACGAATCAGCAGATTGAG 17209
 Qy 426 gaSPMet-----lysMetGlyValIleuPheCysSerCysCysProAspLe 442
 Db 17210 AGAATTATCATCATCAGAAAGAAATGACGATGTTTCCAGTTAAATATTCATGATTC 17269
 Qy 442 uProPheIleTyrAlaPheGlyGlyGlnIlySGLuGly-----IleuAr 456
 Db 17270 TAAATATATTT-----ATCAGTGGATCTGATGATGAGGAAATGTTAGCTATGAGAAAGTAA 17323
 Qy 456 gValITrpAspIleSerThrValIleSerValAsnGlu 468
 Db 17324 AGCTGGAGAGGCTATATGCAAACTACTCTGTA 17360

RESULT 12

US-08-965-600-2
 ; Sequence 2, Application US/08965600
 ; Patent No. 6077688

GENERAL INFORMATION:

APPLICANT: Bandman, Olga
 APPLICANT: Lal, Preeti
 APPLICANT: Corley, Neil C.
 APPLICANT: Shah, Puri
 TITLE OF INVENTION: NEW TRANSDUCIN BETA-1 SUBUNIT
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/965,600
 FILING DATE: Herewith
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0416 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1221 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: KIDN0T02
 CLONE: 194046
 US-08-965-600-2

Alignment Scores:

Pred. No.: 4.2e-10 Length: 1221
 Score: 178.50 Matches: 77
 Percent Similarity: 41.43% Conservative: 56
 Best Local Similarity: 23.99% Mismatches: 125
 Query Match: 6.75% Indels: 63
 DB: 3 Gaps: 15

US-09-315-355C-10 (1-501) x US-08-965-600-2 (1-1221)

Qy 168 ValTyrAsnGlnGluIleuAspSerPheTyrValHisAspIleIleuSerAlaTyr 187
 Db 101 CTCCTCAAAACCAAGCA-----GCCCAATGATGACCAT 136
 Qy 188 ProIleuSerValGluIleuAsnPheAspProSerProAspAspSerThrGlyAsnTyr 207
 Db 137 ---TGCTGCTTCTTGG-----GGACAAACAAAGAAACTGTGAGACA 181
 Qy 208 IleAlaValGlyAsnMetThrProValIleGluValITrpAspIleuAspIleValAspSer 227
 Db 182 GTGTGACAGGCTCCCTAGATGACCTGTGAAGCTCTGG----- 220
 Qy 228 LeuGluProValPheThrIleuGlySerIlySleuSerIlySlySlySlySlySly 247
 Db 221 -----AAATGGCGTGTGAGAGCTGGAC 244
 Qy 248 LysSerSerSerAlaGlnGlyHisThrAspAlaValIleuAspIleuSerITrpAsnIlySleu 267
 Db 245 CTACAGTGAAGTGTGAGGACATCAGCTGGAGGTGTCTGTGACATCGACACACC 304
 Qy 268 IleArgAsnValIleuAlaSerAlaSerAlaAspAsnThrValIleuITrpAspMetSer 287
 Db 305 CTG---CCCATTCCTGATCCAGCTCTCTTGATGCTCATATTCCTTTGGACCTTGAA 361
 Qy 288 LeuGlyIlySProAlaAlaSerIleuAlaValHisThrAspIlySValGlnThrIleuGlnPhe 307
 Db 362 AATGGCAACAGATAAAGTCATAGATGACGAGCTGTGATCTGACCTTGACCTTGCCCTT 421
 Qy 308 HisProPheGluAlaGlnThrIleuIleSerGlySerTyrAspIlySerValAlaIleuTyr 327
 Db 422 TCTCTCT---GATTCACAGATCTGGCCACAGAACTCATGTCCGGAAGTGAACATTTT 478
 Qy 328 AspCysArgSerProAspIlySerHisArgMetITrpArgPheSerGlyGlnIleGluArg 347
 Db 479 GGTGTGAAGTGGAAAAAGAAATATCTTTGGACACAGAGAAATTCATTCTTAGT 538
 Qy 348 ValIThrTrpAsnHisPheSerPro---CysHisPheLeuAlaSer---ThrAspArgIly 365
 Db 539 ATTGCA-----TATAGTCTGTAGGGGAATACCTAGCCAGTGGAGCCATATGGA 589
 Qy 366 PheValITyrAsnIleuAspAlaArgSerAspIlySProIlePheThrIleuAsnAlaHisAsn 385
 Db 590 ATCATCAATATTTTATATTTGCACTGGAAACTTCTGCATCCCTGGAAAGCCATGCC 649
 Qy 386 AspGluIleSerGlyIleuAspIleuSer-----SerGlnIleIlySlyCysIleuValThr 403
 Db 650 ATGCCCATTCGCTCTTGACCTTTCCCGGACTCCAGCTC-----CTTGTCAC 700
 Qy 404 AlaSerAlaAspIlySITyrValIlySileITrpAspIle----- 415
 Db 701 GCTTCAGATGATGGCTACATCAAGATCTATGATGATCAACATGCCAATTTGGCTGGACG 760
 Qy 416 LeuGlyAspArgProSerIleuValHisSerArgAspMetIlySmetGlyValIleuPheCys 435
 Db 761 CTGAGCGGCGCATCCCTCGGTGG-----CTGAACGTTGACATCTGT 802
 Qy 436 SerSerCysCysProAspIleuProPheIleTyrAlaPheGlyGlyGlnIlySGLuGlyIleu 455
 Db 803 CTTGAT-----GACACTCACTTGTTCAGT-----TCGTCTGACAAAGTGA 847
 Qy 456 ArgValITrpAspIleSerThrValIleSerSerValAsnGluAlaPheGlyArgArgGluArg 475
 Db 848 AAAGTTGGAGATTTGGACGAGAGACTGTGTTCACACCTTTTATATCCAGATCCAGATCCAG 907

RESULT 13

US-09-489-506-2
 ; Sequence 2, Application US/09489506
 ; Patent No. 6465619
 ; GENERAL INFORMATION:

APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: NEW TRANSDUCIN BETA-1 SUBUNIT
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/489,506
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/965,600
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0416 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1221 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNOTOT2
CLONE: 194046
US-09-489-506-2

Alignment Scores:
Pred. No.: 4.2e-10 Length: 1221
Score: 178.50 Matches: 77
Percent Similarity: 41.43% Conservative: 56
Best Local Similarity: 23.99% Mismatches: 125
Query Match: 6.76% Indels: 63
DB: 4 Gaps: 15

US-09-315-355c-10 (1-501) x US-09-489-506-2 (1-1221)

Qy 168 ValTyrAengInGUgLUaPserPheTyrValHisHisAlaLeuLeuSerAlaTyr 187
Db 101 CTCCTTCAACAAGACCA-----GCCCATGATGATGCCATT----- 136
Qy 188 ProLeuSerValGUtRPLeuaSnPheAspProSerProAspAspSerThiGlyAsnTyr 207
Db 137 ---TGGTCAGTTCCTTG-----CGACAAACAAGAGAAACTCGAGCA 181
Qy 208 IleAlaValGlyAaMetThrProValIleGluValTTPaPLeuAAspIleValAspSer 227
Db 182 GTGTGCACAGGCTCCCTAGATGACCTGTGAAGCTCG----- 220
Qy 228 LeuGUProValPheThrLeuGlySerLysLeuSerLysLysLysLysLysLysLys 247
Db 221 -----AAATGCGGTGATGAAGGCTGAC 244
Qy 248 LysSerSerSerAlaGluGlyHisThrAspAlaValLeuAAspLeuSerTTPaSnLysLeu 267
Db 245 CTACAGTGAAGTCTGAGAGGACATCAGCTGGAGTGGTCTGTGACATCAGCCACACC 304

Qy 268 IleArgAsnValLeuAlaSerAlaSerAlaAspAsnThrValIleLeuTTPaPLeuSer 287
Db 305 CTG---CCCATTCGTCATCAGCTCTTGCATGCTCATATTCGTCCTTGGAATTGGA 361
Qy 288 LeuGlyLysProAlaAlaSerLeuAlaValHisThrAspLysValGlnThrLeuGlnPhe 307
Db 362 AATGGCAACAGATAAAGTCAATGATGACGAGCCTGTGATCCCTGAGCTTGGCCCTT 421
Qy 308 HisProPheGluAlaGlnThrLeuIleSerGlySerTyrAspLysSerValAlaLeuTyr 327
Db 422 TCTCTT---GATTCCTCAGTATCTGGCCACAGAACTCATGTCGGAAAGTGAACATTTT 478
Qy 328 AspCysArgSerProAspGluSerHisArgMetTyrAspPheSerGlyGlnIleGluArg 347
Db 479 GGTGTGAAGGTGGAAAAAGAAATATCTTGTGACACGAGAGAAATTCATTCTTAGT 538
Qy 348 ValThrTTPaSnHisPheSerPro---CysHisPheLeuAlaSer---ThrAspAspGly 365
Db 539 ATTGCA-----TATAGTCTCTGATGGGAAATACCTACGAGTGGAGCCATAGATGA 589
Qy 366 PheValTyrAsnLeuAspAlaArgSerAspLysProIlePheThrLeuAsnAlaHisAsn 385
Db 590 ATCATCAATATTTTGTATATTCGAACTGGAACCTTCTGCATACCTCGAAGGCCATGCC 649
Qy 386 AspGluIleSerGlyLeuAAspLeuSer-----SerGlnIleLysGlyCysLeuValThr 403
Db 650 ATGCCCATTCGCTTCCTTGACCTTTCCCGGACTCCAGCTC-----CTTGTACT 700
Qy 404 AlSerAlaAspLysTyrValLysIleTTPaPLe----- 415
Db 701 GCTTCAGATGATGCTACATCAAGATCTATGATGATCAATCATCCCAATTTGGCTGGCAGC 760
Qy 416 LeuGlyAspArgProSerLeuValHisSerArgAspMetLysMetGlyValLeuPheCys 435
Db 761 CTGAGCGCCATGCTCTCTGGTG-----CTGAACGTTCGATTTGT 802
Qy 436 SerSerCysAspProAspLeuProPheIleTyrAlaPheGlyGlnLysGluGlyLeu 455
Db 803 CCGTAT-----GACATCATCTTTGTTCCAGT-----TCGTGCAAAAAGTGA 847
Qy 456 ArgValTTPaPLeuSerThrValSerSerValAsnGluAlaPheGlyArgGluArg 475
Db 848 AAAGTTGGGATGTGGAACGAGACCTTGTTTACACACTTCTTGTATCACACGATCAG 907

Qy 476 Leu 476
Db 908 GTC 910

RESULT 14
US-09-620-312D-411
Sequence 411, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aiding J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jians-Rui
APPLICANT: Ma, Yunging
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Fillingnast
APPLICANT: Dymnac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides

```

FILE REFERENCE : 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_FL_genes Version 1.0
SEQ ID NO 411
LENGTH: 2338
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (115) .. (1455)
US-09-620-312D-411

Alignment Scores:
Pred. No.:      1,19e+09      Length:      2338
Score:          178.50       Matches:     105
Percent Similarity: 32.23%   Conservative: 61
Best Local Similarity: 20.39% Mismatches:    207
Query Match:     6.76%      Indels:      143
DB:              4          Gaps:         19

US-09-315-355C-10 (1-501) x US-09-620-312D-411 (1-2338)

Oy      19 LysGIuThrProAspIysValGluLeu-----SerIysGluGluValIysArgLeu 35
        |||:::|||||
Db      59 AAGCAAAACCCGGAGTGAACGCTTTACC GGCGTGTCAGCACGACGAGAGGTTCGAAGTg- 117
Oy      36 IlealglualLysGluIysLeuGlnGluGlyGlyIysSerAspGluGluThr 55
        |||:::|||||
Db      118 GCGGCGCGCAAGGTCGCAGCTCGCACGTGTGA AACCGGGAACCCATGTGAAGCCGAGTCC 177
Oy      56 GlySerProSerGluAspGlyMetGlnSerAlaArgThrGlnAlaArgProArgGluPro 75
        |||:::|||||
Db      178 GCGCAACAAGTTCCAGAGGCCGCCGCCAGGCTACTGCCGCCGCG--GGAGCGCGG 234
Oy      76 LeuGluAspGlyAspProGluAspArgPargThrLeuAspAspAspGluLeuAlaGluTyr 95
        |||:::|||||
Db      235 CTACCGCAAGGG-----GAGAGCTGTGTCATGACGAGAGAGGCTTATGTGCTTAC 285
Oy      96 -----AspLeuAspIysTyrAspGluGlu 103
Db      286 CACCGAGCGCAGACTGTGGCCCCCTGTCTCAGCTTTGACATAAGTCCGG--GATCACTCG 342
Oy      104 GlYasPrProAspAlaGlu-----ThrLeuGlyGlu 113
        |||:::|||||
Db      343 GGAGA CAACCGGACAGAGCTTCTCTTACACTTTACTTGTGTGTGTCGGACCCAGCGTAG 402
Oy      114 Ser-----LeuLeuGlyLeuThrValTyrGlySerAsnAspGlnAspPro 128
        |||:::|||||
Db      403 ACCGGCCAGAGCAACAGACTGATGATGCTTCGATGACATCTGCATGGGACAAAGCCC 462
Oy      129 TyrValThrLeuIysAspThrGlnGlnTyrGluIaArgIuAspPheLeuIleIysProSer 148
        :::|||:::|||||
Db      463 CCACCTCATAGAGGCGCATGATGAAGAAAGAGAGAGAGAT-----504
Oy      149 AspAsnLeuIleValCysGlyArgAlaGluInAspGlnCysAsnLeuGluValHisVal 166
        |||:::|||||
Db      504 -----504
Oy      169 TyrAsnGlnGluIuAspSerPheTyrValHisAspIleLeuLeuSerAlaTyrPro 188
        |||:::|||||
Db      505 -----GAAGAGGATGAAGAGAGCGGAACCTCAGCTGAGCTGGCCATAGTCC 555
Oy      189 -----LeuSerValGluTrpLeuAsnPheAspProSerProAsp 201
        :::|||:::|||||
Db      556 CACTATGTGGCATCAACGAGAGTTCGGGTCTACGTGGGTGAAGG-----603
Oy      202 AspSerThrGlyAsnTyrIleAlaValGlyAsnMetThrProValIleGluValTyrAsp 221

```

```

Dh 604 -----CTGTGGCTGGGGTGTGCA 624
Qy 222 -----LeuapllValAspSerIeu 228
Dh 625 GAGNAGGGCCAGGTGAGTGTTCGCGTCGCGGCTTTCGACAGTGTGTGAGAGGCC 684
Qy 229 GluProValPheThrIleuGlySerIleuSerIylsIylsIylsIylsGlyIyls 248
Dh 685 CAGGCGCTG-----GACGCTTCCCTCCGGGATGAGCGGCCCAATATAGGCC 732
Qy 249 SerSerSerIaGluGlyIsthrAspAlaValIleuAspLeuSerTrpAsnIylsIle 268
Dh 733 ATCTTCCTCTTCGTGTGACATGTGGGAGGCGCTTCCTTACTGATGTGTCGCCCGGGGT 792
Qy 269 ArgAsnValIleuAlaSerAlaSerAlaAspAsnThrValIleuTrpAspMetSerIeu 288
Dh 793 ACCGTCGCTGTGTACCGGTGACTGTCAAAAGACATCACCTCTGGACACTACGAC 852
Qy 289 Gly-----LysProAlaAlaSerIleuAlaValIsthrAspIys 301
Dh 853 GGGCGCTCTTGACGACGTGACCAAGCGGCTCATTCGTGGGC-----CACACGCTCT 903
Qy 302 ValGlnThrIleuGlnPheIstProPheGluAlaGlnThrIleuIleSerGlySerTrp 321
Dh 904 GTGAGGACCTTCGACGTGTACCGACTGAGAACACGCGTGTGCTCTCTGTCACTGAC 963
Qy 322 LysSerValAlaLeuTrpAspCySarIserProAspIuSerIstAspMet----- 338
Dh 964 GCGTCATCGCATCTGGACATCCGGGACGCCCGGACCGCCAGAGCGCTGATCTCACACA 1023
Qy 339 ---TrpArgPheSerGlyGlnIleGluArgValThrTrpAsnIstPheSerProCysHis 357
Dh 1024 GCCACCGCCCATGTAGGGAGCATGTCATGTCATGCTGAGCGCCCGGGAGGCC--TTC 1080
Qy 358 PheIleuAlaSerThrAspAspGlyPheValTyrrAsnIleuAspAlaArg-----Ser 374
Dh 1081 CTGCTTCGTGGCGGGAGTGAATGGGCGCCCTCAAGATCTGGAGCTTCGGCAGTTCAAGCT 1140
Qy 375 AspIysProIlePheThrIleuAsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSer 394
Dh 1141 GGTCCCCACAGTGGCCATTCGACAGCAGCAGTGCGCCCGGACCTCGTGAGTGGCAC 1200
Qy 395 SerGlnIleIysGlyCysLeuValThrAlaSerAlaAspIylsTyrrValIylsIleTrpAsp 414
Dh 1201 CCCGAGGACAGCGGGGTCTTTGACGCTCGGGTGCAGACCAACGATCACACAGTGGGAC 1260
Qy 415 Ile-----LeuGlyAsp 418
Dh 1261 CTGGCACTGAGCGGACCTGTAGCGGGCGCATGTGAGCGGACCCCGACTGGCCGAC 1320
Qy 419 ArgProSer-----LeuValHisSerArgAspMetIylsMetGlyValIleuPheCys 435
Dh 1321 CTCCCGACGACGCTGCTGTTCGTGCACACAGGCGCAGACCGAGCTGAGAGACTGCAC 1380
Qy 436 SerSerCysProAspLeuProPheIleTyrrAlaPheGlyIly 450
Dh 1381 CACCGCAGTGCACGAGGCTCTCTGTGACAGCAGCGCTGTGAGGC 1425

RESULT 15
US-09-108-857-1
; Sequence 1, Application US/09108857A
; Patent No. 6433137
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, Alexander D.
; APPLICANT: BRAUN, Burkhard
; TITLE OF INVENTION: TUP1 SEQUENCES FROM CANDIDA ALBICANS AND METHODS FOR
; TITLE OF INVENTION: SCREENING AGENTS FOR INHIBITING VIRULENCE IN CANDIDA
; FILE REFERENCE: 22002-20006.00
; CURRENT APPLICATION NUMBER: US/09/108, 857A
; CURRENT FILING DATE: 1998-07-01
; EARLIER APPLICATION NUMBER: 60/051,552
;

```

EARLIER: FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2272
TYPE: DNA
ORGANISM: Candida albicans
FEATURE:
NAME/KEY: CDS
LOCATION: (337)..(1878)
US-09-108-857-1

Alignment Scores:
Pred. No.: 4,07e-09 Length: 2272
Score: 173.50 Matches: 115
Percent Similarity: 35.21% Conservative: 73
Best Local Similarity: 21.54% Mismatches: 181
Query Match: 6.57% Indels: 165
DB: Gaps: 26

US-09-315-355c-10 (1-501) x US-09-108-857-1 (1-2272)

QY 26 GluLeuSerlysgluValIyAlaArgLeuIleAlaGluAlaIyGluIyLeuGluGlu 45
DB 550 GAGGCATACGAGAGAGATTGAGGTTAAAGACGATTGACACTAGACAGACGCAA 609
QY 46 GluGlyGlySerAspGluGluGluThrGlySerProserGluAspGlyMetGlnSer 65
DB 610 ATGAAGATGGCTTCCAAACAACAAGACAGACAAACAAGACAAACAAGACAG 669
QY 66 AlaArgThrGln-----AlaArgProArgGluProLeuGluAspGlyAspProGlu 82
DB 670 CAGCAACAACAAGATTGTGGACCAACCTGCCGCCACCTGCTCCACCAACCCG--- 726
QY 83 AspAspArgThrLeuAspAspAspGluLeuAlaGluTyrAspLeuAspGlyTyrAspGlu 102
DB 726 ----- 726
QY 103 GluGlyAspProAspAlaGluThrLeuGlyLeuSerLeuGlyLeuThrValTyrGly 122
DB 727 -----GTCACATCTATTATCG 741
QY 123 SerAsnAspGlnAspProTyrVal-----ThrLeuIyAspThrGluGlnTyrGlu 139
DB 742 GTTATGACAGACGACATACATATTGTCAACCCCAAGAGGTAACACGTCAGAGAA 801
QY 140 ArgGluAspPheLeuIleIyAspProserAspAsnLeuIleValCysGlyArgAlaGluGln 159
DB 802 ATCCACCATCTCTG-----CAAGATTAGCATTTGCCAAAGCCCAACCCGAGTTC 852
QY 160 AspGlnCysAsnLeuGluValIleVal-----TyrAsnGlnGluGluAsp 174
DB 853 AAGAAACAGACCTCGAATACATATGTGTGTAACAACCGAGGTCTCCAAAGACTTGAT 912
QY 175 SerPheTyrValIleIyAsp-----HisAspIleLeuSerAlaTyrProLeuSerVal 191
DB 913 ATTGACATGCTCCACTCTTAGACCACTGTCAGTGTTCCTGCGAGATTTCCAGA 972
QY 192 GluTyrLeuAsnPheAspProserProAspAspSerThrGlyAsnTyrIleAlaValGly 211
DB 973 GAC-----GGCAAGTTTCATCGCCACCGGT 996
QY 212 -----AsnMetThrProValIleGluValTyrAspLeuAspIleValAspSerLeuGlu 229
DB 997 TGCAACAACACCCCAAGTTCATGTCACACCGGAGAGTGTGTC----- 1044
QY 230 ProValPheThrLeuGlySerIySerIySerIySerIySerIySerIySer 249
DB 1045 -----GCCAATTTGATTGACAGATCTCCCAAGAAACAA----- 1080
QY 250 SerSerAlaGluGlyHisThrAspAlaValLeuAspLeuSerTyrAsnIySerLeuIleArg 269
DB 1081 -----GACGACAAACACCGCTCAGGCGACTTG-----TACATCGA 1119

QY 270 AsnVal-----LeuAlaSerAlaSerAlaAspAsnThrVal 281
DB 1120 TCTGTGTGTTTCTCCCTGACGGAACCTTGGCAGACAGGTGCAGACAGATGATT 1179
QY 282 IleLeuTyrAspMetSerLeuGlyIySerProAlaAlaSerLeuAlaValIleThrAspIyS 301
DB 1180 AGAATCTGGGATTGAGCACAAAGAAATTAATCTTGGAGGGCCCAAGAACAGAC 1239
QY 302 ValGlnThrLeuGlnPheHisProPheGluAlaGlnThrLeuIleSerGlySerTyrAsp 321
DB 1240 ATTTACTGTTTAACATTTTCCCT---GATGGCATAGTGTGTTTCAGGCTCCGCGAT 1296
QY 322 IySerValAlaLeuTyrAspCysArg----- 330
DB 1297 AGGTCAAGTCAAGATCTGGGACCTTGAGAACCTCCAGATGTTCTTGACTTGTGATCGAA 1356
QY 331 -----SerProAspGluSerHisArgMetTyrAspPheSer 342
DB 1357 GACGGCGTCAACACCGTGGCCGTCTCCCGGACGGA-----CTCATGTGCTGCC 1407
QY 343 GlyGlnIleGluArgVal-----ThrTyrAsnHisPheSerProCysHisPheLeuAla 360
DB 1408 GGCTCATATGATGAACCGTTAGAGTGTGGAC----- 1440
QY 361 SerThrAspAspGlyPheValTyrAsnLeuAspAlaArgSerAspIySerProIlePheThr 380
DB 1441 TCACACTACGGGCTTCTGGTGCAGAACCTTAGATCCGGCAACGAAACGCG----- 1491
QY 381 LeuAsnAlaHisAsnAspGluIleSerGlyLeuAspLeuSerGlnIleIyGlyCys 400
DB 1492 ---AATGGCCACCAAGATTCAGTCTACTGTGCTCTTCCCAACAACGCGCAACA--- 1545
QY 401 LeuValThrAlaSerAlaAspIySerTyrValIySerIleTyrAspIleLeuGly-----Asp 418
DB 1546 ATGCTTCGGGCTCTTAGACAGAACCGTCAAGTGTGGCATTTGGACCAAGCTCCGAC 1605
QY 419 ArgProSer-----LeuValHisSerArgAspMetIySerGlyValLeu 433
DB 1606 AAAAAGTCGACCTCGGAGGTACCTTACCTTGGCCACAGACCTTGTGTGCGGTC--- 1662
QY 434 PheCysSerSerCysCysProAspLeuProPheIleTyrAlaPheGlyGlnIyGlu 453
DB 1663 -----TGCTGTACCCCGCAACGAGTACATTTTGTGCG---GGCTCAAGGACCGT 1710
QY 454 GlyLeuArgValIleAspIleSerThrValSerSerValAsnGluAlaPheGlyArgArg 473
DB 1711 GGTCATTTTCTGGGAC-----CAAGCTTACGAT---AAC 1743
QY 474 GluArgLeuValIleGlySerAlaArgAsnSerSerIleSer----- 487
DB 1744 CCAATTGTGATGTTGACGGGCGCAACCGAATCGGTATCTCACTCGCTGTATCCCTTAAC 1803
QY 488 -----GlyProPheGlySerArgSerSerAsp 496
DB 1804 TCAAGGGAACGAAAGTATCTTCGTACACGATGTGCGCAT 1845

Search completed: January 31, 2004, 04:27:38
Job time : 142 secs

From: Chan, Christina
Sent: Thursday, January 29, 2004 11:25 AM
To: Holleran, Anne; STIC-Biotech/ChemLib
Subject: RE: RUSH search for 09/315,355

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Holleran, Anne
Sent: Thursday, January 29, 2004 10:36 AM
To: Chan, Christina
Subject: RUSH search for 09/315,355

Please approve and forward to STIC the following RUSH sequence search. This is for an amendment due this biweek. Thanks.

Please search the following in the interference search databases:

1. polynucleotides that encode SEQ ID NO: 10
2. oligomer search of polynucleotides that encode SEQ ID NO: 10

Anne Holleran
AU: 1642
Tel: 308-8892
RM: 8e03

mailbox: 8e12

After Jan. 30:

Tel: 571 272-0833
RM: Remsen, 3A14

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 2/2
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

